Aar60789 HTV virus Aar60783 HTV virus Abu07696 Viral coa Aab61506 HTV-1 del Abr57053 HTV-1 JR-AdK14401 HTV gp140 Abu07697 Viral coa Abb1505 HTV-1 SOS Abr57052 HTV-1 JR-Abr57052 HTV-1 JR-Abr57052 HTV-1 JR-Adk14399 HTV env g Adk14399 HTV env g Adk14399 HTV env g Adk14499 Viral coa Abu07694 Viral coa Abu07694 Viral coa Abu07695 Viral coa Adk14404 HTV mutan Adk14405 HTV mutan

Viral coa HIV virus HIV virus

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This sequence represents a human immunodeficiency virus type 1 (HIV-1) envelope (env) protein amino acid sequence. The invention relates to the HIV-1 env protein or its fragments, which when administered to a mammal, induces the production of broadly cross-reactive neutralising anti-serum against multiple strains of HIV-1. The HIV-1 env protein and its fragments are useful as vaccines, immunogenic compositions or disagnostic reagents. They can also be used to detect anti-HIV-1/HIV-1 neutralizing antibodies in a sample. The amino acid sequence and its fragments or mRNA sequence are useful for generating antibodies in a mammal, In addition, a recombinant delivery vector containing the env amino acid sequence may also be used as a vaccine. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus-1 envelope protein, useful as a vaccine or immunogenic preparation against HIV-1 infection induces the production of broadly cross-reactive neutralizing anti-serum.
                                                                                                                                                                                                                                                                                                                    HIV-1; envelope protein; env; cross reactive anti-serum; antibody; vaccine; antibody; detect.
                                                                                                                                                                                                                                                                                                    HIV-1 envelope protein amino acid sequence.
                                                                                                                                                                                            ALIGNMENTS
                       AAR60789
AAR60783
ABC0783
ABC0765
AABC1506
ABC1506
ABC1506
ABC1506
ABC1607697
ABC1607697
ABC1309
ABC1309
ABC14309
ABC07694
ABC07694
ABC14389
ABC07694
ABC07694
ABC07694
ABC07694
                                                                                                                                                                                                                                        AAY79020 standard; protein; 866 AA
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                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (JACK-) JACKSON FOUND HENRY M.
                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0095267P.
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                                                                                                                                                                                                                                                                          (revised)
(first entry)
Quinnan GV, Zhang PF;
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WO200007631-A1.
                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1999;
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05-JUN-2000
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AAY79020;
                                                                                                                                                                                                                               AAY79020
S HIV-1 JR-
5 Novel ant
HIV-1 gp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV-1 gp1
HIV-1 JR-
HIV env g
HIV-1 str
HIV-1 iso
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PND EE8378
PND EE669
PND EE322
PND EE238
PND EE533
PND EE533
PND EE533
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Aay79023 HIV-1 RV
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                                                          April 11, 2005, 10:37:31 ; Search time 11.7951 Seconds (without alignments) 1180.438 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Aar20912
Aar20910
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Aar68028 |
Abb07702 |
Abb5702 |
Abr57050 |
Abr57050 |
Abr18104 |
Adf18104 |
Adf74742 |
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Aab69350
Aar20883
Aar20953
Aar20853
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Aar29113
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         5.1.6
Compugen Ltd.
                                                                                                               1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCN 36
                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                          2105692 seqs, 386760381 residues
                                                                                         US-09-762-261C-1_COPY_301_336
201
         GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                           - protein search, using sw model
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AAR20912
AAR20910
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AAR20883
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Gapop 10.0 , Gapext 0.5
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geneseqp2003bs:*
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length: 2000000000
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Match Length
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RESULT 2

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Novel genomic nucleic acids of non-subtype B human immunodeficiency virus type 1 useful for detecting and treating AIDS comprises a specific
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                                                                                                                                                                      HIV-1; human immunodeficiency virus; non-subtype B; gag; pol; env; vpu; vlf; vpr; tat; rev; nef; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV; PND; principal neutralising determinant; Omp; Neisseria; outer membrane proteosome; AIDS; vaccine; envelope gene.
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Pred. No. 3.2e-16;
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                                                                                                                                   HIV-1 non-subtype B clone 93BR029-4 env protein.
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AAB69350 standard; protein; 842 AA.
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88.9%;
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Matches 32; Conservative
                                                                             (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type 1 useful for de
nucleotide sequence.
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20-APR-2001
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                                      AAB69350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a human immunodeficiency virus type 1 (HIV-1) R2 strain envelope (env) protein V3 region peptide sequence. The invention relates to the HIV-1 env protein or its fragments, which when administered to a mammal, induces the production of broadly crossreactive neutralising anti-serum against multiple strains of HIV-1. The HIV-1 env protein and its fragments are useful as vaccines, immunogenic compositions or diagnostic reagents. They are also be used to detect anti-HIV-1/HIV-1 neutralizing antibodies in a sample. The amino acid sequence and its fragments or mRNA sequence are useful for generating antibodies in a mammal, In addition, a recombinant delivery vector containing the env amino acid sequence may also be used as a vaccine. (Updated on 12-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus-1 envelope protein, useful as a vaccine or immunogenic preparation against HIV-1 infection induces the production of broadly cross-reactive neutralizing anti-serum.
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                                      Length 866;
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                                                                           Indels
                                                                                                                                      301 CSRPNNNTRKSIPMGPGRAFYTTGOIIGDIROAHCN 336
                                  Score 201; DB 3;-
pred. No. 4.4e-18;
mismatches 0;
                                                                                                                 1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCN 36
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                                  100.0%;
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(first entry)
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                                                                           Conservative
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                Query Match
Best Local Similarity
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Matches 35; Conserv
Sequence 866 AA;
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Gaps

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Indels

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19-FEB-1992.

RESULT 3

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The sequences represented in AAQ21054-61, AAQ21194-311 and AAQ21321-78 encode PNDs of HIV (envelope protein) which are useful as immunogens for AIDS vaccines, partic. in the form of conjugates. To prepare antigenic conjugates, PND (of HIV) and Omp (of Neisseria) are prepd. separately, then linked by cross-linking agents, monogeneric spacers or bigeneric spacers. The conjugate may comprise 1-50 PNDs. A PND has 15 amino acids or less, but at least 5, it contains Gly-X-Gly, where X is Pro, Leu, Ala, Gln or Ser. The conjugates as AIDS or HIV vaccines can be used prepost-exposure to prevent or treat HIV infection or disease, and are capable of producing an immune response specific for the immunogen. See also AAQ21052-61, AAQ21051-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                    New antigenic conjugate of HIV major neutralisation determinant - covalently linked to outer membrane proteosome of Neisseria, useful a vaccine and in treating and preventing HIV infections, AIDS and ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     covalently linked to outer membrane proteosome of Neisseria, useful vaccine and in treating and preventing HIV infections, AIDS and ARC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV; PND; principal neutralising determinant; Omp; Neisseria; outer membrane proteosome; AIDS; vaccine; envelope gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.0%; Score 185; DB 2; Length 35; 91.4%; Pred. No. 2.3e-17; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CTRPNNNTRKSIPIGPGRAFYTTGEIIGDIRQAHC 35
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                                                                                                                            Claim 1; Page 175 + 168; 177pp; English
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90US-00566654.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 32; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 35 AA;
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                                                                                                                                                                                                                                                                                                    New antigenic conjugate of HIV major neutralisation determinant - covalently linked to outer membrane proteosome of Neisseria, useful as vaccine and in treating and preventing HIV infections, AIDS and ARC.
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outer membrane proteosome; AIDS; vaccine; envelope gene.
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                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 175 + 117-118; 177pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
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                                                               90US-00566638.
                      91EP-00202025
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90US-00566656
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90US-00566656
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N-PSDB; AAQ21298.
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Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35 AA;
                      07-AUG-1991;
                                                             13-AUG-1990;
13-AUG-1990;
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                                                                                                        13-AUG-1990;
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Query Match

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EP471407-A

AAR20953;

RESULT 5 AAR20953

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then linked by cross-linking agents, monogeneric spacers or bigeneric spacers. The conjugate may comprise 1-50 PNDs. A PND has 35 amino acids or less, but at least 5, it contains Gly-X-Gly, where X is Pro, Leu, Ala, Gln or Ser. The conjugates as AIDS or HIV vaccines can be used pre- or post- exposure to prevent or treat HIV infection or disease, and are capable of producing an immune response specific for the immunogen. See also AAQ21052-61, AAQ21194-311 and AAQ21321-78
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                                                                                                                                                                      Length 35;
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                                                                                                                                                                      Score 185; DB 2; L
Pred. No. 2.3e-17;
3; Mismatches 0;
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90US-00566654.
90US-00566656.
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91.4%;
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1 Similarity 91.4%;
32; Conservative
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N-PSDB; AAQ21232.
                                                                                                                                      Sequence 35 AA;
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Best Local 9
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Best Local Similarity

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covalently linked to outer membrane proteosome of Neisseria, useful as
vaccine and in treating and preventing HIV infections, AIDS and ARC.
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                                                                                                                                                                                                                                  Neisseria;
gene.
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35
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Pred. No. 4.2e-17;
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1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC
                 1 CTRPNNNTRKSIPIGPGRAFYTTGDIIGDIROAHC
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90US-00566656.
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Best Local Similarity 91.4%;
Matches 32; Conservative
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13-AUG-1990;
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(first entry)

01-JUN-1992

PND EE228-2

90US-00566654. 90US-00566638.

13-AUG-1990; 13-AUG-1990; 13-AUG-1990;

(MERI ) MERCK & CO INC Lewis JA, Davide JP, WPI; 1992-058471/08. N-PSDB; AAQ21233.

91EP-00202025.

07-AUG-1991;

19-FEB-1992 EP471407-A.

Human immunodeficiency virus

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The sequences represented in AAQ21054-61, AAQ21194-311 and AAQ21321-78 encode PNDs of HIV (envelope protein) which are useful as immunogens for ADS vaccines, partic. in the form of conjugates. To prepare antigenic conjugates, PND (of HIV) and OMP (of Neisseria) are prepar entigenic conjugates, PND (of HIV) and OMP (of Neisseria) are prepar suringenic paperers. The conjugate may comprise 1:50 PNDs. A PND has 35 amino acids or less, but at least 5, it contains Gly-X-Gly, where X is Pro, Leu, Ala, Gln or Ser. The conjugates as AIDS or HIV vaccines can be used pre- or pacyent or treat HIV infection or disease, and are capable of producing an immune response specific for the immunogen. See also AAQ21052-61, AAQ21194-311 and AAQ21321-78
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covalently linked to outer membrane proteosome of Neisseria, useful as
vaccine and in treating and preventing HIV infections, AIDS and ARC.
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Pred. No. 4.2e-17;
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91.4%; Pred. No. 4...
... 2; Mismatches
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                                         07-AUG-1991;
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19-FEB-1992
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antigenic conjugate of HIV major neutralisation determinant -covalently linked to outer membrane proteosome of Neisseria, useful as vaccine and in treating and preventing HIV infections, AIDS and ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                   determinant; Omp; Neisseria; vaccine; envelope gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
91.0%; Score 183; DB 2; Length 35;
Best Local Similarity 91.4%; Pred. No. 4.2e-17;
Matches 32; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 175 + 65; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterbury JA;
                                                                                                 HIV; PND; principal neutralising outer membrane proteosome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR20912 standard; protein; 35
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Human immunodeficiency virus

EP471407-A

(first entry)

01-JUN-1992

AAR20912;

RESULT 10 AAR20912

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PND EE533-3

Sequence 35 AA;

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WPI; 1992-058471/08.

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The sequences represented in AAQ21054-61, AAQ21194-311 and AAQ21321-78 encode PNDs of HIV (envelope protein) which are useful as immunogens for ALDS vaccines, partic. in the form of conjugates. To prepare antigenic conjugates, PND (of HIV) and Omp (of Neisseria) are prepd. separately, then linked by cross-linking agents, monogeneric spacers or bigeneric spacers. The conjugate may comprise 1-50 PNDs. A PND has 35 amino acids or less, but at least 5, it contains Gly-X-Gly, where X is Pro, leu, Ala, Gln or Ser. The conjugates as AIDS or HIV vaccines can be used pre- or post- exposure to prevent or treat HIV infection or disease, and are capable of producing an immune response specific for the immunogen. See also AAQ21052-61, AAQ21194-311 and AAQ21321-78
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                                                  New antigenic conjugate of HIV major neutralisation determinant - covalently linked to outer membrane proteosome of Neisseria, useful vaccine and in treating and preventing HIV infections, AIDS and ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antigenic conjugate of HIV major neutralisation determinant - covalently linked to outer membrane proteosome of Neisseria, useful vaccine and in treating and preventing HIV infections, AIDS and ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV; PND; principal neutralising determinant; Omp; Neisseria; outer membrane proteosome; AIDS; vaccine; envelope gene.
                                                                                                                                                                                                                                                                                                                                                                                                   91.0%; Score 183; DB 2; 91.4%; Pred. No. 4.2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 175 + 139-140; 177pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 175 + 66; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterbury JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR21136 standard; protein; 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-00566638.
90US-00566654.
90US-00566656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-058471/08.
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Best Local Similarity
                N-PSDB; AAQ21334
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 35 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
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conjugates, PND (of HIV) and Omp (of Neisseria) are prepd. separately, then linked by cross-linking agents, monogeneric spacers or bigeneric spacers. The conjugate may comprise 1-50 PNDs. A PND has 35 amino acids or less, but at least 5, it contains Gly-X-Gly, where X is Pro, Leu, Ala, Gln or Ser. The conjugates as ALDS or HIV vaccines can be used pre- or pacyene to prevent or treat HIV infection or disease, and are capable of producing an immune response specific for the immunogen. See also AAQ21052-61, AAQ21194-311 and AAQ21321-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Principle neutralising determinant peptide(s) of HIV gp120 protein - used for diagnosing, preventing and treating HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8. .14
/note= "classification of PND peptides is determined by
the predicted secondary structure of this region - see
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Principal Neutralising determinant; Human immunodeficiency virus; vaccine; Robson's analytical method; polymerase chain reaction; Garnier-Osguthorpe-Robson method; GOR method; secondary structure.
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                                                                                                                                                                                                     91.0%; Score 183; DB 2; Length 35; 91.4%; Pred. No. 4.2e-17; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                   1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC 35
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/note= "conserved PND motif"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KAGA ) CHEMO SERO THERAPEUTIC RES INS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Group II HIV gp120 PND peptide 8926C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       AAR29113 standard; protein; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 10; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                           32; Conservative
                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-400517/49.
                                                                                                                                                                   Sequence 35 AA;
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02-APR-1993
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2; Mismatches

Length 35; Indels HIV receptor; V3 loop; retrovirus; P95 protein; nucleolin; P30 protein; PHAPI; P40 protein; PHAPII; infection; therapy; diagnosis.

HIV-1 Ba-L isolate V3 loop

(revised)
(first entry)

15-MAR-1999 17-OCT-2003

AAW84056;

6 CTRPNNNTRKSIQIGPGRAFYTTGEIIGDIRQAHCN 41

AAW84056 standard; peptide; 39 AA.

RESULT 15

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Groups I, II and III). Group II PND peptides are those which have the structure XXBBBBX on the amino-terminal side of the GPGR motif (B = betastrand structure and X = turn or coil structure). Vaccine preparations comprising representative peptides from each of the 5 groups can be used to develop vaccines able to recognise any HIV variant. See AAQ31607-Q31608, AARR8995-R29000 and AAR29110-R29128. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New protein comprising the V3 sequence of 62.19 in the context of Con6 gpl20, useful in preparing a composition for inducing the production of neutralizing antibodies against HIV.
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                                                                                                                                                                                    Length 35;
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                                                                                                                                                                                                                       Indels
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Best Local Similarity 91.4%; Pred. No. 4.2e-17;
Matches 32; Conservative 2; Mismatches 1;
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                                                                                                                                                                                                                                                         1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC 35
                                                                                                                                                                                                                                                                            CTRPNNNTRKSIPIGPGRAFYTTGDIIGDIRQAHC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel anti-HIV compound-related peptide #101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 40; 49pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                ADR58150 standard; protein; 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2003; 2003US-00373592.
08-MAY-2003; 2003US-00431596.
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Best Local Similarity
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                                                                                                                                                 Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated V3 loop HIV receptor - comprises P95/nucleolin, P40/PHAPII and P30/PHAPI proteins, used to develop products for the treatment and prevention of HIV infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Muller
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Pred. No. 6.4e-17;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Krust B, Jacotot E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CTRPNNNTRKSIHIGPGRAFYTTGEIIGDIRQAHCN 37
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                                                                                                                                                                                                          Human immunodeficiency virus 1; isolate Ba-L.
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Job time : 14.7951 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                     Callebaut C,
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                                                                                                                                                                                                                                                                                                                                                                   (INSP ) INST PASTEUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39 AA;
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91.0%; Score 183; DB 8; Length 45; 88.9%; Pred. No. 5.5e-17; ive 3; Mismatches 1; Indels

1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCN 36

Conservative

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                           US-09-762-261C-1_COPY_301_336
201
1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCN 36
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                         283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
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T09448
S13289
S35859
S35820
S35820
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PC2296
C412296
C412396
S35835
S35835
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S35850
H44001
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                      length: 0
length: 2000000000
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Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
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envelope protein (V3 domain) - human immunodeficiency virus type 1 (fragment) cispecies: human immunodeficiency virus type 1, HIV-1 cispecies: human immunodeficiency virus type 1, HIV-1 cispecies: human immunodeficiency virus type 1, HIV-1 cispecies: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004 C;Accession: A46410 R;McNearney, T.; Hornickova, Z.; Markham, R.; Birdwell, A.; Arens, M.; Saah, A.; Ratner, Protein A.; Hornickova, Z.; Markham, R.; Birdwell, A.; Arens, M.; Saah, A.; Ratner, A.; Title: Relationship of human immunodeficiency virus type 1 sequence heterogeneity to st A;Reference number: A46410; MUID:93066216; PMID:1438212

RESULT 2

90.5%; Score 182; DB 2; Length 110;

Query Match

A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid
A;Residues: 1-110 <MCNN
A;Cross-references: UNIPROT:Q9PY06
A;Cross-references: UNIPROT:Q9PY06
A;Experimental source: subject S1
A;Note: sequence extracted from NCBI backbone (NCBIP:117724)
C;Superfamily: type E retrovirus env polyprotein

	30 11	175	87.1	7.7	77	842	S42918 S45821	env polyprotein -	
	1 CI EI	174	86.6	7.7	0 0	835	S35824 S35825	envelope protein - envelope protein -	
	) W (	174	86.6	110	10	046	D46410	envelope protein (	
	36	173	86.1	71	- 7	842	VCLUBR S42904	env polyprotein -	
	37	173	86.1	17 12	7	842	2905 2898	env polyprotein - env nolyprotein -	
	36	173	86.1	77	101	835	5815	envelope protein -	
	0 4 0 L	172	85.6	506 35	~ ~	PC2	A40218 PC2297	envelop glycoprote V3 domain peptide	
	42	171	85.1	77	7	835	835800	envelope protein -	
	4, 4 4, 4	171	85.1	200	N 0	23.5	\$35801 \$60529	envelope procein -	
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						•	ALIGNMENTS		
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	envelope protein	proteir	mnų - u	un immu	nod	lefic	-	(strain CSF2951) (fragment)	
	C;Species C;Date: 0	1: numar 16-Feb-1	1995 #se	oderici equence	enc re	y vy visiv	C.Species: numan immunodeficiency Virus Cype 1, Alv-1 C.Date: 06-Feb-1995 #sequence revision 06-Feb-1995 #text_change 09-Jul-2004	_change 09-Jul-2004	
	R, Chiodi, F.	F. 33.	, 7000	,0000	0				
	submitted to the EMBL Data A:Reference number: 835800	l to the	e EMBL I	Data Li 5800	bra	ry,	submitted to the EMBL Data Library, June 1993 A:Reference number: 835800		
	A, Accession: S35862	on: 835	5862						
	A;Status: preliminary A:Molecule twoe: DNA	prelin	ninary						
′	A;Residues: 1-77 <chi></chi>	18: 1-77	· CHI						
	A: Experim	eference	ces: UNJ	PROT:Q	775 CS	44; F295	A;Cross-references: UNIPROT:Q77544; UNIPROT:Q77542; UNIPROT:Q77545; A:Rxnerimental source: strain CSF2951 clone3: strain CSF2951 clone4	ROT:Q77545; EMBL:Z23246; NID:g31: 2951 clone4	ID:9313
	A, Accession: S35860	on: 83	2860		;	) 	-		
	A;Status: preliminary	prelin	ninary						
	A; Residues: 1-77 <ch2></ch2>	8: 1-7	7 <ch2></ch2>						
	A;Cross-r A:Experim	eferenc	ses: EME	3L:Z232 strain	44; CS	NID F295	A;Cross-references: EMBL:Z23244; NID:g313631; PIDN:CAA80762.1; A:Experimental source: strain CSF2951 clone11; strain CSF2951	A;Cross-references: EMBL:Z23244; NID:g313631; PIDN:CAA80762.1; PID:g313632; EMBL:ZZ3247; A:Experimental source: strain CSF2951 clone11; strain CSF2951 clone4	23247;
	C; Superfa	mily: t	ype E	retrovi	ru8	env	Superfamily: type E retrovirus env polyprotein		
	Query Match Best Local	Tatch Scal Sim		90.5%; ilarity 88.9%;	10 Q 46 46	۰	Score 182; DB 2; Leng Pred. No. 2.8e-18;	Length 77;	
	Marcines			נימרדים		· ·	i	o' carre	
	ò	1 20 -	SRPNNNTF	RKSI PMG	PGR =	AFYT	CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCN 36		
	qa	26 CT	TRPNNNTF	KSINIG	PGR	AFYT	CTRPNNNTRKSINIGPGRAFYTTGEIIGDIRQAHCN 61		

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Page

32; Conservative

Best Local Similarity Matches 32, Conserv

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A,Cross-references: UNIPROT:Q77541; EMBL:Z22243; NID:g313629; PIDN:CAA80761.1; PID:g3136:
C;Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-77 <CHI>
A;Cross-references: UNIPROT:Q77501; UNIPROT:Q77538; EMBL:Z23200; NID:g313546; PIDN:CAA807
C;Superfamily: type E retrovirus env polyprotein
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V3 domain peptide P4346 - human immunodeficiency virus type 1 (fragment)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Species: Luseb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C;Accession: PC2296

C;Accession: PC2296

R;Sherefa, K.; Soennerborg, A.; Steinbergs, J.; Saellberg, M.

Biochem. Biophys. Res. Commun. 205, 1658-1664, 1994

A;Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotyping A;Reference number: PC2291; MUID:95110306; PMID:7811250
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C,Species: human immunodeficiency virus type 1, HIV-1
C,Bate: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C,Accession: 835819; 835856
R,Chiodi, F.
Submitted to the EMBL Data Library, June 1993
A,Reference number: 835800
A,Accession: 835819
A,Status: preliminary
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                                                                                           90.0%; Score 181; DB 2; Length 76; 88.9%; Pred. No. 3.8e-18; Live 2; Mismatches 2; Indels
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90.0%; Score 181; DB 2; Length 77;
Best Local Similarity 88.9%; Pred. No. 3.9e-18;
Matches 32; Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                           1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCN 36
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Pred. No. 3.9e-18;
2; Mismatches 2;
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                                                                                                                       Best Local Similarity 88.9
Matches 32; Conservative
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Matches 32; Conservative
  A;Residues: 1-76 <CHI>
                                                                                                  Query Match
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S35820
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S35819
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R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A
Nature 348, 69-73, 1990
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A;Reference number: S13288; MUID:91043044; PMID:2172833
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: S38859; S35871
R;Chiodi, F.
submitted to the EMBL Data Library, June 1993
A;Reference number: S35800
A;Accession: S35859
A;Accession: S35859
A;Accession: Library, June 1993
A;Accession: S35859
A;Accession: S36859
A;Accession: S36859
A;Accession: S36859
A;Accession: S36859
                                                                                                                                                                                                                                         envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Cross-references: UNIPROT:Q75760; EMBL:U63632; NID:g1465777; PID:g1465781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       env protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
                           Gaps
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                           Indels
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Pred. No. 3.5e-17;
3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 182; DB 2; L Pred. No. 3.5e-17; 3; Mismatches 1;
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                                                                                                1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCN 36
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88.9%; Pred. No. 4.1e-18; ative 3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T09448
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-847 <PAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Residues: 1-847 <OBR>
A,Cross-references: UNIPROT:Q75760
C,Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    env polyprotein
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Query Match
Best Local Similarity 88.9%;
Matches 32; Conservative

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A,Gene: env C,Superfamily: type E retrovirus

C, Genetics:

90.5%;

Query Match Best Local Similarity 88.9° Matches 32; Conservative

RESULT 5 S35859

A; Status: preliminary

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A;Status: preliminary
A;Status: breliminary
A;Molecule type: DNA
A;Residues: 1-77 <CHI>
A;Residues: 1-77 <CHI>
A;Coss-references: UNIPROT:Q77530; EMBL:Z23232; NID:g313607; PIDN:CAA80750.1; PID:g3136(
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                                                                                                                        envelope protein - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: S35835
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61
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Pred. No. 7.4e-18;
1; Mismatches 3;
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Pred. No. 7.4e-18;
26 CTRPNNNTRKSIHMGPGRAFYATGDIIGDIRQAHCN
                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-77 <CHI>
A;Cross-references: UNIPROT:Q77518; EMBL:223218
C;Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q77517; EMBL:Z23217 C;Superfamily: type E retrovirus env polyprotein
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                                                                                                                                                                                                                                                R;Chiodi, F.
submitted to the EMBL Data Library, June 1993
A;Reference number: 835800
A;Accession: 835836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Richiodi, F. submitted to the EMBL Data Library, June 1993 A;Reference number: 835800 A;Accession: 835835
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88.9%;
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Best Local Similarity 88.9%;
Matches 32; Conservative
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A;Accession: S35848
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Best Local Similarity
Matches 32; Conserv
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A;Molecule type: DNA
A;Residues: 1-77 <CHI>
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A,Note: this virus was isolated from the mother's sexual partner
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C;Superfamily: type B retrovirus env polyprotein
C;Superfamily: type B retrovirus env polyprotein
C;Superfamily: type B retrovirus env polyprotein; immunodeficiency; polyprotein-
C;Superfamily: capacing protein gpl20 (fragment) #status predicted <GP1>
F;1-251/Product: coat protein gp41 (fragment) #status predicted <GP2>
F;252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F;424-443/Pomain: transmembrane #status predicted <TMN>
F;9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: c:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A. Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A;Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity A;Reference number: A41621; MUID:92107924; PMID:1763038
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N;Alternate names: coat polyprotein
N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C;Species: human immunodeficiency virus type 1, HIV-1
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C;Superfamily: type E retrovirus env polyprotein
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995; #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: S35834; S35837
S;Chiodi, F
submitted to the EMBL Data Library, June 1993
A;Reference number: S35800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: host Homo sapiens (man)
C;Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
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88.9%; Pred. No. 3.3e-17;
tive 2; Mismatches 2; Indels
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                                                                                                                                                                    Length 35;
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91.4%; Pred. No. 2.3e-18;
tive 2; Mismatches 1;
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                       A,Molecule type: protein
A,Residues: 1-35 <SHE>
A,Cross-references: UNIPROT:Q70831
C,Superfamily: type E retrovirus env polyprotein
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Matches 32; Conservative
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les 32; Conserv
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A; Residues: 1-443 <BUR>
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A; Residues: 1-77 < CHI>
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A, Status: preliminary
A; Accession: PC2296
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Subsequence in the forman immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Reb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: S35849
R;Chiodi, F.
Submitted to the EMBL Data Library, June 1993
A;Reference number: S35800
A;Accession: S35849
A;Accession: S35849
A;Accession: S35849
A;Accession: S35849
A;Accession: MINEQT:Q77531; EMBL:Z23233; NID:g313609; PIDN:CAA80751.1; PID:g3136
C;Superfamily: type E retrovirus env polyprotein
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1 CSRPNNVTRKSIPMGPGRAFYTTGQIIGDIRQAHCN 36
                                       26 CTRPNNNTRKGIHIGPGRAFYTTGEIIGDIRQAHCN 61
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S35849
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envelope protein - human immunodeficiency virus type 1 (fragment) C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004 RESULT 15

26 CTRPNNNTRESIHIGPGRAFYTTGEIIGDIRQAHCN 61

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1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCN 36

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Sichiodi, F.
Submitted to the EMBL Data Library, June 1993
Submitted to the EMBL Data Library, June 1993
Sykeference number: 835800
A; Reference number: 83587
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-77 < CHI>A; CHI
A; Cross-references: UNIPROT: Q77539; EMBL: Z23241; NID: 9313625; PIDN: CAA80759.1; PID: 93136
C; Superfamily: type E retrovirus env polyprotein

Query Match 88.6%; Score 178; DB 2; Length 77; Best Local Similarity 86.1%; Pred. No. 1e-17; Matches 31; Conservative 3; Mismatches 2; Indels

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Search completed: April 11, 2005, 11:15:28 Job time : 2.72785 secs

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Q8aiw7 Q9q865 Q68y25 Q68y26 Q68y27 Q68y28 Q68y29 Q68y29

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SEQUENCE FROM N.A.
MEDLINE=99236722; PubMed=10221533; DOI=10.1089/088922299311088;
Quinnan G.V. Jr., Zhang P.F., Fu D.W., Dong M., Alter H.J.;
"Expression and characterization of HIV type 1 envelope protein
associated with a broadly reactive neutralizing antibody response.";
AIDS Res. Hum. Retroviruses 15:561-570(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
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Quinnan G.V. Jr., Zhang P.F., Fu D.W., Dong M., Alter H.J.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; API29126; AAD40637.3; -.

EMSP; P04578; 1DLB.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral capsid; IEA.

GO; GO:001931; C:viral envelope; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR000328; ENV GP41.
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039362;
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Last annotation update)
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Q9PXN8
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Q90056
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Pfam; PF00517; GP41; 1.
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              GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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090205
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Q79067
Q9DPV9
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Q8AEX6
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Q78198
Q8AIV5
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Gapóp 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 2000000000
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Match Length DB
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Perfect score:
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MEDLINE=21084776; PubMed=11216936;
WEDLINE=21084776; MESTAN MESTA
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EMBL, AJ228189; CAA12819.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
FIREPROPER, GPL20, 1.
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Pred. No. 5.9e-20;
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                                                          090956 PRELIMINARY, PRT; 85 AA. 090956; 0.1-NOV-1998 (TEMBLrel. 08, Created) 01-NOV-1998 (TEMBLrel. 08, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) 09120 (Fragment).
                                                                                                                                                                                                                                                                                            Human immunodeficiency virus 1.
Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676,
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1-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNA-2003 (TrEMBLrel. 12, Last annotation update)
Envelope glycoprotein (Fragment).
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NCBL_TaxID=11676;
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Matches 34; Conservative
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Lukashov V.V. Kuiken C.L., Boer K., Goudsmit J.;
"HIV type I subtypes in The Netherlands circulating among women
originating from AIDS-endemic regions.";
AIDS Res. Hum. Retroviruses 12:951-953 (1996).
EMBL; L76886; AAC37946.1;
EMBL; L76886; AAC37946.1;
GO; GO:001691; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:001918; F:structural molecule activity; IEA.
InterPro; IPR00077; GP120.
Pfam; PF00516; GP120; 1.
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                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-98242906; PubMed-9583604;
Lukashov V.V., Op de Coul E.L., Coutinho R.A., Goudsmit J.;
"HIV-1 strains specific for Dutch injecting drug users in heterosexually infected individuals in The Netherlands.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 98.5%; Score 198; DB 2; Length 91; Local Similarity 97.2%; Pred. No. 2.4e-20; tes 35; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                        AIDS 12:635-641(1998).

EMBL, AF032157, AAC59382.1, -
60, Go:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:00198; F:structural molecule activity; IEA.

InterPro; IPR000777; GP120.

Pfam; PF00516; GP120.
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VDL_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Last annotation update)
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1; Mismatches
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STRAIN=R923572;
MEDLINE=96392168; PubMed=8798980;
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SEQUENCE FROM N.A.
MEDLINE=9402215; PubMed=8415653;
Kulken C.L., Zwart G., Baan E., Coutinho R.A., Hoek van den J.A.R.,
Goudamit J.;
Pfam, PF00516; GP120; I.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=990931; PubMed=9824326; MEDLINE=990932; PubMed=9824326; Goudamit J., Lukashov V.V., van Ameijden E.J., Zorgdrager F., van den Burg R., Cornelissen M. "Impact of sexual versus parenteral transmission events on the evolution of the gag and env genes of HIV type 1."; AIDS Res. Hum. Retroviruses 14:1483-1486(1998). "EMBL; ARC71286; AAC71738.1; -... GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0019031; C:viral capaid, IEA. GO; GO:0019031; C:viral envelope; IEA. GO; GO:0005198; F:structural molecule activity; IEA.
                                                                                                          Score 194; DB 2; Length 92;
Pred. No. 9e-20;
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Pred. No. 9e-20;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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InterPro; IPR007110; Ig-like.
                                                                                                        96.5%;
94.4%;
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1 Similarity 94.4%;
34; Conservative
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Best Local Similarity
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Wang X.-P., Kahn P.D., Cunha C.B., Dosik D.A., Gawel C., Kaplan M.H.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; A337523; AAQ83712.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.
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MEDLINE=99039932; PubMed=9824326;
Goudsmit J., Lukashov V.V., van Ameijden E.J., Zorgdrager F.,
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBL_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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      Pred. No. 6.2e-20;
2; Mismatches 0;
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                                                                  1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCN 36
                                                                                             97.0%; Score 195; DB 2; 94.4%; Pred. No. 1.3e-19;
                                                                                                                                                                                                                       171 AA
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      Best Local Similarity 94.4%;
Matches 34; Conservative
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Pfam; PF00516; GP120; 1.
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"Increasing antigenic and genetic diversity of the HIV-1 V3 domain in the course of the AIDS epidemic"."; Proc. Natl. Acad. Sci. U.S.A. 90:9061-9065(1993).
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EMBL, AF291142; AAG35348.1; -.

GO, GO:0019028; C:viral capsid, IEA.

GO, GO:0019031; C:viral capsid, IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:005198; F:structural molecule activity; IEA.

InterPro; IPR000777; GP120.

Pfam; PF00516; GP120; I.

AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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                                                                                                                                                                MEDLINE=96203966; PubMed=8627267; Kuiken C.L., Cornelissen M.T.E., Zorgdrager F., Hartman S., Gibbs A.J., Goudsmit J.; Gibbs A.J., Goudsmit J.; Consistent risk group-associated differences in human immunodeficiency virus type 1 vpr, vpu and V3 sequences despite independent evolution."; J. Gen. Virol. 77:783-792(1996).
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Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0019028; C:viral cappid; IEA.
R GO; GO:0019031; C:viral envelope; IEA.
R GO; GO:0005198; F:structural molecule activity; IEA.
R GO; GO:0005199; F:structural molecule activity; IEA.
R InterPro; IPR000777; GP120.
R InterPro; IPR007110; IQ-like.
R InterPro; IPR007110; IQ-like.
R Pfam; PF00516; GP120; 1.
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Best Local Similarity 94.4%; Pred. No. 1.1e-19;
Matches 34; Conservative 2; Mismatches 0; Indels
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112 AA; 12603 MW; A2F0458A21E5C6E2 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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EMBL, AR291141; AAG35347.1; -.

EMBL, AR291141; AAG35347.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:005198; F:structural molecule activity; IEA.

InterPro; IPR00077; GP120.

PEAM: PF00516; GP120; II.

AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral envelope; IEA.
GO; GO:0019031; F:structural molecule activity; IEA.
GO; GO:0019031; F:structural molecule activity; IEA.
InterPro; IPR000777; GP120.
AIDS; Coat profein; Envelope protein; Glycoprotein; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang Y.M., Saksena N.K.;
"Molecular evidence for drug-induced compartmentalizaion of HIV-1
quasispecies in a patient with periodic changes to the HAART
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112 AA; 12587 MW; 16E8F2D91CBB6AEE CRC64;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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NCBI_TaxID=11676;
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1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCN 36
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                              28 CTRPNNNTRKSIPIGPGRAFYTTGQIIGDIRQAHCN
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Score 194; DB 2; Length 112; Pred. No. 1.1e-19; 2; Mismatches 0; Indels

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GO, GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro: IPR00777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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112 AA; 12586 MW; A2E8F2D91CBB7034 CRC64;
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Best Local Similarity 94.4%; Pred. No. 1.1e
Matches 34; Conservative 2; Mismatches
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Matches 34; Conservative
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"Molecular evidence for drug-induced compartmentalization of HIV-1
quasispecies in a patient with periodic changes to the HAART
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Mang Y.M., Saksena N.K.;
"Molecular evidence for drug-induced compartmentalizaion of HIV-1 quasispecies in a patient with periodic changes to the HAART
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112 AA; 12585 MW; A2E8F2D911D6C6E2 CRC64;
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GO; GO:0016021; C:integral to; IEA.
GO; GO:0019028; C:virtal capsid; IEA.
GO; GO:0019031; C:virtal envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPRO0577; GP120.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                                                                   Ouery Match 96.5%; Score 194; DB 2; L
Best Local Similarity 94.4%; Pred. No. 1.1e-19;
Matches 34; Conservative 2; Mismatches 0;
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AIDS 0:0-0(2001).
EMBL, #5291138; AAG35344.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
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MEDLINE=95194719; PubMed=7888212;
Kalish M.L., Luo C.C., Weniger B.G., Limpakarnjanarat K., Young N.,
Ou C.Y., Schochetman G.;
"Early HIV type I strains in Thailand were not responsible for the current epidemic.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeally A.R.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U15579; AGC54014.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019198; F:structural molecule activity; IEA.
InterPro; IPR000777; GB120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein, C2-V3 region (Fragment).
                                                                                                                                                                                                                            Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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113 AA.
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PRT;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

April 11, 2005, 10:37:31 ; Search time 283.737 Seconds (without alignments) 1180.438 Million cell updates/sec Run on:

US-09-762-261C-1

Perfect score:

4617 1 MRVKGIRRNYQHWMGWGTML......GRALLHIPTRIRQGLERALL 866 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A\_Geneseq\_16Dec04:\* 1: genesecm1980er\*

geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2002s:\*

geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Aay79020 HIV-1 env	Aar14904 HIV-1 (MN-	Aaw11580 Human Imm	Aaw88112 Predicted	Aaw11579 Human Imm	Aaw88111 Predicted	Adp04371 Envelope	2	Aar79173 HIV virus	Aab82761 Ancestral	Aar14903 HIV-1 (MN)	Aaw43068 HIV-1 gp1	Abr55495 Amino aci	Adp04369 Envelope	Adk14406 HIV wild-	Adp20081 Human imm		Aar67724 gp120 fro	Adk14405 HIV mutan	Adp20072 Human imm		Aaw88113 Env prote	Aar67725 gp120 fro	Aay97073 Variant H	Ado05103 Human imm
ΠD	AAY79020	AAR14904	AAW11580	AAW88112	AAW11579	AAW88111	ADP04371	AAW58805	AAR79173	AAB82761	AAR14903	AAW43068	ABR55495	ADP04369	ADK14406	ADP20081	ADK14404	AAR67724	ADK14405	ADP20072	AAW11581 .	AAW88113	AAR67725	AAY97073	AD005103
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Score	4596	3971.5	3971.5	3971.5	3970	3970	3941.5	3935	3933	3920.5	3917	3913	3896	3859.5	3845.5	3845.5	3841.5	3841	3839.5	3814	3812.5	3812.5	3806.5	3795.5	3795.5
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Aap80967 HIV prote	Aar67726 gp120 fro		Aao19389 Lymphaden	Aar25940 Modified	Aab85999 Amino aci	Aar43869 HTLV-III	Ado52541 HIV-1 rec	Aap60422 Seguence	Aap60063 HIV virus	Aap60349 HTLV-III	Aap70665 Sequence	Ado52531 HIV-1 rec	Aaw89325 HIV-1 env	Abu63322 Human lym	Ado26434 HTLV-III	Aaul1872 HIV env p	Aay97072 Wild type		Adn36425 HIV prote
AAP80967	AAR67726	AAW43069	AA019389	AAR25940	AAB85999	AAR43869	AD052541	AAP60422	AAP60063	AAP60349	AAP70665	AD052531	AAW89325	ABU63322	AD026434	AAU11872	AAY97072	ADE84721	ADN36425
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82.0	81.6	81.4	81.3	81.1	81.1	81.1	81.0	80.9	80.9	80.9	80.9	80.8	80.8	80.8	80.8	80.7	80.7	80.7	80.7
3787.5	3768	3758.5	3753.5	3744	3744	3744	3738.5	3735.5	3734.5	3734	3733.5	3732.5	3731	3731	3731	3726.5	3726	3726	3726
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

HIV-1 envelope protein amino acid sequence. AAY79020 standard; protein; 866 AA (revised)
(first entry) 12-SEP-2003 05-JUN-2000 AAY79020; THE STATE OF THE S

HIV-1; envelope protein; env; cross reactive anti-serum; antibody; vaccine; antibody; detect.

Human immunodeficiency virus 1.

WO200007631-A1

17-FEB-2000.

99WO-US017596. 04-AUG-1999; (JACK-) JACKSON FOUND HENRY M.

04-AUG-1998; 98US-0095267P.

Zhang PF; Quinnan GV,

WPI; 2000-205578/18.

Human immunodeficiency virus-1 envelope protein, useful as a vaccine or immunogenic preparation against HIV-1 infection induces the production of broadly cross-reactive neutralizing anti-serum.

Claim 2; Page 33; 54pp; English.

This sequence represents a human immunodeficiency virus type 1 (HIV-1) envelope (env) protein amino acid sequence. The invention relates to the HIV-1 env protein or its fragments, which when administered to a mammal, induces the production of broadly cross-reactive neutralising anti-serum against multiple strains of HIV-1. The HIV-1 env protein and its fragments are useful as vaccines, immunogenic compositions or diagnostic reagents. They can also be used to detect anti-HIV-1/HIV-1 neutralizing antibodies in a sample. The amino acid sequence and its fragments or mRNA sequence are useful for generating antibodies in a mammal, In addition, a recombinant delivery vector containing the env amino acid sequence may also be used as a vaccine. (Updated on 12-SEP-2003 to standardise OS

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US HIV-1 isolates MN-ST1 and BA-L, ENV protein and DNA - are useful in therapeutics, vaccines and diagnostic tests.
                                                                                           human immunodeficiency virus; United States; MN isolate; AIDS
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                                                                      env protein
           (revised)
(revised)
(revised)
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25-MAR-2003
17-DEC-2001
05-FEB-1992
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                                  Score 4596; DB 3;
Pred. No. 2.6e-243;
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Best Local Similarity 99.5%;
Matches 862; Conservative
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The infectious molecular clone, lambda MN-ST1, was obtained by cloning integrated provirus from DNA purified from peripheral blood lymphocytes integrated with HIV-1(NN) and maintained in culture for one month. The integrated proviral DNA was partially digested with Sau3A to give fragments of 15-20 kb. The fragments were cloned in EMBL3 and the entire sequence of the clone was determined and the amino acid sequence of the env protein was deduced from it. (Note: Revised entry submitted to correct the parent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further www.derwent.com/dwpi/updates/ntis us.html.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
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86.6%; Pred. No. 3.7e-209;
iive 37; Mismatches 70;
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                                               TIVFNQSSGGDPEIVMHSFNCGGEFFYCNTSPLFNSTWNG-NNTWN-----NTTGSNNNI
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25-MAR-1997
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25-FEB-1993;
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Markham PD;
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         New isolated envelope protein of HIV-1 strain BA-L and recombinant equivalents - useful as immunogens for vaccines and antibody producypical of US clinical isolates.
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86.6%; Pred. No. 3.7e-209;
ive 37; Mismatches 70; Indels
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                                            840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding env protein of the human immune deficiency virus isolate BA- L - useful for producing protein for use in vaccines, as assay reagent and to generate antibodies.
GYSPLSFQTRLPAPRGPDRPERIEEEGGDRDRDRSGLLVDGFLTLIWVDLRSLCLFSYHR 780
                    771
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            712 GYSPLSLQTRPPVPRGPDRPEGIEEEGGERDRDTSGRLVHGFLAIIWVDLRSLFLFSYHH
                                                         772 LRDLLLIAARIVELLGRRGWEVLKYWWNLLQYWSQELKSSAVSLLNATDIAVAEGTDRVI
                                            781 LRDLLLIVTRIVELLGRRGWEILKYWWNLLQYWSQELKNSAVSLFNATAIAVAEGTDRVI
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                                                                                                                                                                                                                                               Predicted amino acid sequence of the MN-ST1 envelope (env) protein
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93US-00022835.
95US-00388809.
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                                                                                      LTPLCVTLNCTDLRNTTNTNNSTANNNSNSEGTIKGGEMKNCSFNITTSIRDKMQKEYAL
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The present sequence represents the predicted amino acid sequence of the MN-PH1 clone envelope (env) protein. MN-PH1 is a Human immunodeficiency virus type 1 (HIV-1) clone. The specification also describes the env and rev coding sequences of the HIV-1 strain BA-L (ATCC 40890). BA-L is more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding env protein of the human immune deficiency virus isolate ^{1} . useful for producing protein for use in vaccines, as assay reagent
                                                                                   601 LLGIWGCSGKLICTTTVPWNASWSKNKTLEAIWNNMTWMQWDKEIDNYTSLIYSLIEESP
                                                                                                                                             661 IQQEKNEQELLELDKWANLWNWFDISNWLWYIKIFIMIVGGLVGLRIVFVVLSIVNRVRQ
                                                                                                                                                                                                  712 GYSPLSLQTRPPVPRGPDRPEGIEEEGGERDRDTSGRLVHGFLAIIWVDLRSLFLFSYHH
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                                                                                                                                                                                                                                          GYSPLSFQTRLPAPRGPDRPEEIEEEGGDRDRDRSGLLVDGFLTLIWVDLRSLCLFSYHR
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                                                                                                                                                                                                                                                                                                                                                                                                               The permuted circular unintegrated viral DNA representing the complete HIV-1(MN) genome was cloned into the EcoRI site of lambda gtWES.lambda B DNA from total DNA of H9 cells producing HIV-1(MN) isolate. The clone was designated lambda MN-PH1 The present sequence was deduced from the env gene region of the MN-PH1 genome. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DTEVHNVWATQACVPTDPNPQEVELVNVTENFNMWKNNMVEQMHEDIISLMDQSLKPCVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 LYKLDIVSIDNDSTSYRLISCNTSVITQACPKISFEPIPIHYCAPAGFAILKCNDKKFSG 240
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                                                                                                                                                                                                                                                                                                                             New isolated envelope protein of HIV-1 strain BA-L and recombinant equivalents - useful as immunogens for vaccines and antibody prodn. typical of US clinical isolates.
                                                                                                                                                                                                                                            Gartner
                env
                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 86.0%; Score 3970; DB 2; Length 856; Local Similarity 86.7%; Pred. No. 4.5e-209; nee 751; Conservative 36; Mismatches 69; Indels 10
                                                                                                                                                                                                                                            Popovic M, Reitz MS,
              immune deficiency syndrome; AIDS; envelope
                                                      Human immunodeficiency virus 1; (strain MN-PH1)
                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                          Lori FC,
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                                                                                                                                                                    90US-00599491
93US-00022835
                                                                                                                                          95US-00388809
                                                                                                                                                                                                                                          Franchini G,
                                                                                                                                                                                                                                                                                    WPI; 1997-011206/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 856 AA;
                                                                                                                                          15-FEB-1995;
                                                                                                                                                                                   25-FEB-1993;
                                                                                                                                                                      17-OCT-1990;
                                                                                                                                                                                                                                         Gallo RC, F
Markham PD;
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typical of United States isolates of HIV-1 than previously known strains. Recombinant, complete env protein of the BA-L strain is used as a vaccine component and for immunotherapy of existing HIV infections, to detect HIV specific antibodies, e.g. in donated blood, and as an immunogen to raise specific antibodies, for HIV-1 diagnosis. (Updated on 17-OCT-2003 to
                                                                                                                                                                                                                                                                                                                             61 DIEVHNVWATQACVPIDPNPQEVELVNVIENFNWMKNNNVVEQMHEDIISLMDGSLKPCVK 120
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                                                                                                                                                                                                                                                                      1 MRVKGIRRNYQHWWGWGTMLLGLLMICSATEKLWVTVYYGVPVWKEATTTLFCASDAKAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREERAVGLGAMFFGFLGAAGSTMG
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                                                                                                                                                                                                   Gaps
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                                                                                                                                                              Length 856;
                                                                                                                                                                                                   Indels
                                                                                                                                                              86.0%; Score 3970; DB 2;
86.7%; Pred. No. 4.5e-209;
ive 36; Mismatches 69;
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                                                                                                                                                              Query Match
Best Local Similarity 86.7
Matches 751; Conservative
                                                                                          standardise OS field)
                                                                                                                             Sequence 856 AA;
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The invention relates to a method of identifying a human immunodeficiency virus type-1 (HIV-1) envelope protein which produces a cross-reactive immune response following administration in a mammal by: (a) substituting one or more amino acids in or near the gp41, CD4-binding, co-receptorbinding or outer domains of gp120; and (b) identifying one or more amino acid substitutions in the domains that produce a cross-reactive immune response following administration in a mammal. The method is useful for identifying an HIV-1 envelope protein, which produces a cross-reactive immune response following administration in a mammal. Compositions comprising such HIV-1 envelope protein may be used as HIV subunit vaccine or immunogenic composition that can induce antibodies that neutralize HIV strains across different phenotypes and clades, or for the prevention or therapy of HIV-1 infection. This sequence corresponds to the gp120 envelope glycoprotein from a neutralisation antibody-sensitive (T-cell line adapted) MN strain of HIV-1 (MN-P).
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                                                                                                                                                                                anti-HIV; vaccine; human immunodeficiency virus type-1; envelope glycoprotein; cross-reactive immune response; gp41; CD4-binding; co-receptor-binding; outer domain; gp120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying an HIV-1 envelope protein that produces a cross-reactive immuna response in a mammal, comprises introducing amino acid substitutions into gpl20, and identifying substitutions that produce cross-reactive immune response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9;
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                                                                                                                                             Envelope protein gp120 from antibody sensitive HIV strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.4%; Score 3941.5; DB 85.7%; Pred. No. 1.6e-207; ive 46; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 4; 68pp; English.
                                  Ä.
                                  protein; 857
                                                                                                                                                                                                                                                           Human immunodeficiency virus 1.
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                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2002; 2002US-0379052P.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (JACK-) JACKSON FOUND HENRY
                                                                                                         26-AUG-2004 (first entry)
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                                                                                                                                                                                                                                                                                             WO2004045495-A2
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Disclosure; Fig 1; 25pp; English
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                                                                         KGSCKNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSENFTNNAKTIIVQLREPVKIN
                                                                                                                                                                                                                                                       361 TIVFNPSSGGDPEIVMHSFNCGGEFFYCNTSPLFNSTWNG-NNTWN-----NTTGSNNNI
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CD4-binding region; anti-HIV antibody; therapeutic; infection;
inhibition; T cell; immunogenic agent; antibody; vaccine; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        801. .855 // /note= "region with MHC II homology"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401. .800
/label= CD4_binding_region
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/label= v3 loop
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This sequence represents the Human Immunodeficiency Virus Type I (HIV-I) isolate MN envelope protein gpl20. This protein is used in a novel method to produce and analyse peptides oligomers, "peptomers", consisting of several peptide monomers arranged head to tail, each monomer comprising a sequence from a CD4-binding region of HIV gpl20. Such peptides are useful as assay reagents for detecting anti-HIV antibodies in biological samples, e.g. blood samples, or as a therapeutic agent for inhibiting infection of T cells by HIV and as an immunogenic agent for inhibiting and thus are consistent in their sequence and structure. Most HIV vaccines and detection peptides used currently rely on fragments of inactivated live viruses and thus may not contain the correct epitopes to elicit an immune response. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                 diagnostic, immunogenic or
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86.1%; Pred. No. 3.7e-207;
ive 36; Mismatches 74;
                                                              Harris-Kelson TA
                                                                                                                                                                                                 HIV gp120 peptide oligomers - useful as
(USSH ) US DEPT HEALTH & HUMAN SERVICES
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us-09-762-261c-1.rag

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Peptide analogues of HIV virus antigen contain a plurality of peptide monomers, each comprising the gpl20 CD4 binding region consensus sequence (amino acids 419-436) (see AAR79172). The synthetic peptomers are useful as therapeutic agents, immunogens in vaccine compositions or for the diagnosis of disease. Since the analogues maintain the conformation of the native proteins from which they are derived (the consensus sequence), they are useful against infection by various HIV-1 and HIV-2 isolates (see AAR79174-84)
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Pred. No. 4.7e-207;
                                                                                                                                                                                                                                                                                                                                                                               37; Mismatches
                                         Disclosure, Fig 1; 55pp; English
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86.0%;
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gp120 peptide.
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GGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREERAVGLGAMFFGFLGAAGSTMG
                         GGDMRDNWRSELYKYKVVTIEPLGVAPTKAKRRVVQREKRA-AIGALFLGFLGAAGSTWG
                                                                                                                                                                             LLGIWGCSGKLICTTTVPWNASWSKNKTLEAIWNNMTWMQWDKEIDNYTSLIYSLIEESP
                                                                                                                                                                                                      LIGEWGCSGKLICTTTVPWNASWS-NKSLDDIWNNMTWMQWEREIDNYTSLIYSLLEKSQ
                                                                                                                                                                                                                                                                   IQQEKNEQELLELDKWANLWNWFDISNWLWYIKIFIMIVGGLVGLRIVFVVLSIVNRVRQ
                                                                                                                                                                                                                                                                                              TQQEKNEQELLELDKWASLWNWFDITNWLWYIKIFIMIVGGLVGLRIVFAVLSIVNRVRQ
                                                                                                                                                                                                                                                                                                                                                             GYSPLSFOTRLPAPRGPDRPEEIEEEGGDRDRDRSGLLVDGFLTLIWVDLRSLCLFSYHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -RDLLLIAARIVELLGRRGWEVLKYWWNLLQYWSQELKSSAVSLLNATAIAVAEGTDRVI
                                                                                       AASVTLTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQ
                                                                                                            LRDLLLIVTRIVELLGRRGWEILKYWWNLLQYWSQELKNSAVSLFNATAIAVAEGTDRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV virus-1; gp120; therapeutic; immunogen; diagnostic; peptomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "MHC II homology region consensus
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419. .436
/note= "CD4 binding region (801. .856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of an ancestral HIV-1 group M, subtype B gp160 (env gene product) sequence. The invention provides compositions and methods for determining ancestral viral gene sequences and ancestral viral protein sequences for highly diverse viruses, such as HIV-1. The methods use samples of circulating viruses to determine an ancestral case, the ancestral HIV-1 subtype B env sequence (see AAH26468) was determined using 38 subtype B env sequence (see AAH26468) was determined using 38 subtype D (outgroup) sequences. The distances between this ancestral viral sequence and circulating strains used to determine it were on average 12.3% (range: 80-21.0%) while the available specimens were 17.3% different from each other (range: 13.3-23.2%). Thus, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           circulating virus than to any other variant. The ancestral gp160 sequence included a wide variety of immunogenically active peptides when processed for antigen presentation; nearly all known subtype B CTL epitope consensus amino acids were represented. Thus, an immunogenic composition to this subtype B ancestor protein will elicit broad neutralising antibody against HIV-1 isolates of the same subtype, and will also elicit a broad cellular response mediated by antigen-specific T-cells. A claimed vaccine composition comprises a viral ancestor protein or its immunogenic fragment, especially one derived from the HIV-1 group M subtype B gp160 ancestral protein. (Updated on 11-SBP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preparing an ancestral viral amino acid sequence useful as a vaccine comprises determining a recent ancestor of a circulating virus by maximum
-RDLLLIAARIVELLGRRGWEVLKYWWNLLQYWSQELKSSAVSLLNATAIAVAEGTDRVI 830
                                                                                                                                                                                                                                                               HIV-1; env gene; gp160 protein; ancestral gene; phylogeny; vaccine.
                                                                                                                                                                                                                                   Ancestral HIV-1 group M, subtype B gp160 protein.
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                                                                                                                                                                                                                                                                                            Human immunodeficiency virus 1.
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(first entry)
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29-OCT-2001
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Gaps 12;

Indels 29;

Query Match 84.9%; Score 3920.5; DB 4; Length 883; Best Local Similarity 84.5%; Pred. No. 2.3e-206; Matches 751; Conservative 43; Mismatches 66; Indels 29;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     698 IVGGLVGLRIVFVVLSIVNRVRQGYSPLSFQTRLPAPRGPDRPEEIEEEGGBRDRBGL
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                                                                                                                                                                                                                                                175 OKEYALLYKLDIEPIDND-----NTSYRLISCNTSVITQACPKISFEPIPIHYCAPAGF
                                                                                                                                                                                                                                                                                                                                229 AILKCNDKKFSGKGSCKNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSENFTNNAKT
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                                                                                 DTEAHNVWATHACVPTDPNPQEVELVNVTENFNWWKNNMVEQMHEDIISLWDQSLKPCVK
1 MRVKGIRRNYQHWWGWGTMLLGLLMICSATEKLWVTVYYGVPVWKEATTTLFCASDAKAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      818 KNSAVSLFNATAIAVAEGTDRVIQVLQRVGRALLHIPTRIRQGLERALL 866
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652 TQQEKNEQELLELDKWASLWNWFDITNWLWYIKIFIMIVGGLVGLRIVFAVLSIVNRVSQ
                                                                                                                                                                                                                                                                                                                                                                                                    474 GGDMRDNWRSELYKYKVVTIEPLGVAPTKSKRRVVQREKRA-AIGALFLGFLGAAGSTWG
                                                                                                                                                                                                                                                                                                  661 IQQEKNEQELLELDKWANLWNWFDISNWLWYIKIFIMIVGGLVGLRIVFVVLSIVNRVRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         781 LRDLLLIVTRIVELLGRRGWEILKYWWNLLQYWSQELKNSAVSLFNATAIAVAEGTDRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -RDLLLIAARIVELLGLRGWEFLKYWWNLLQYWSQELKSSAVSLLNATAIAVAEGTDRVI
                                                               481 GGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREERAVGLGAMFFGFLGAAGSTMG
                                                                                                                                           AASVTLTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQO
                                                                                                                                                                               533 AASVTLTVQARLLLSGIVQQQNNLLRAIEAQQHMLQLTVWGIKQLQARVLAVERYLKDQQ
                                                                                                                                                                                                                        LLGIWGCSGKLICTTTVPWNASWSKNKTLEAIWNNMTWMOWDKEIDNYTSLIYSLIEESP
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94US-00240073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The permuted circular unintegrated viral DNA representing the complete HIV-1 (MN) genome was cloned into the EcoRI site of lambda grWES.lambda B DNA from total DNA of H9 cells producing HIV-1 (MN). This clone was designated lambda MN-H1; it was subcloned in M13mpl8 and M13mpl9 and the DNA sequence of the entire clone was obtained the amino acid sequence of the enverte the protein was deduced from it. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further www.dervent.com/dwpi/updates/ntis us.html.) (Updated on 25-MRR-2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                              US HIV-1 isolates MN-ST1 and BA-L, ENV protein and DNA - are useful in therapeutics, vaccines and diagnostic tests.
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                        MN isolate; AIDS
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Local Similarity 85.7%; Pred. No. 3.5e-206;
Les 742; Conservative 40; Mismatches 74; Indels 1
                        human immunodeficiency virus; United States;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 3; 61pp; English
                                                                                 Human immunodeficiency virus 1,
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fractionating a crude gp120 preparation containing full-length, glycosylated gp120 using ion exchange chromatography so as to provide a glycosylated gp120 using ion exchange chromatography so as to provide a selected that exhibits specific binding affinity for CD4 peptide, thereby producing a first fractionated material. The first fractionated material is fractionated by hydrophobic interaction chromatography so as to provide a second collection of fractions from which a second collection is selected that exhibits specific binding affinity for CD4 peptide. This second fraction is fractionated by size exclusion chromatography so as to provide a third collection of fractions exhibiting specific binding affinity for CD4 peptide, thereby providing the purified gp120. The purified gp120 can be used for antibody production and in vaccines. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 GGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRVVQREERAVGLGAMFFGFLGAAGSTMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 AASVTLTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLGIWGCSGKLICTTVPWNASWSKNKTLEAIWNNMTWMQWDKEIDNYTSLIYSLIEESP
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                                                                                                                                                                                                                                                                                                        1 MRVKGIRRNYQHWWGWGTMLLGLLMICSATEKLWVTVYYGVPVWKEA-TTLFCASDAKAY
                                                                                                                                                                                                                                                                                                                                                                                                          120 LTPLCVTLNCTDLRNTTNTNNSTANNNSNSEGTIKGGEMKNCSFNIYTSIRDKMQKEYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 TIVENOSSGGDPEIVMESFUCGGE-FYCNTSPLFNSTWNGNNSTWN-----NTTGSNNNI
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                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                       84.8%; Score 3913; DB 2; Length 854;
86.1%; Pred. No. 5.8e-206;
ive 35; Mismatches 73; Indels 12
                                                                                                                                                                                                                                                   Conservative
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les 746; Conserv
                                                                                                                                                                                               Sequence 854 AA;
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The specification describes a method of determining the influence of variation in host genes on selection of microorganisms with protein substitutions. The method comprises typing all individuals of a substitutions. The method comprises typing all individuals of a substitutions. The method substitutions at least one selected intrinsic polymorphic marker involved in the host response to the presence of the microorganism. The method is useful for examining selective pressures confronting a wide range of organisms that exhibit pathogenic traits in a host, such as bacteria, fungi, mycobacterium, confronting and protein mycobacterium, confronting and protein mycobacterium, confronting and selective pressures such as HCV and HBV. The method is useful for hepatitis related viruses such as HCV and HBV. The method is useful for designing a vaccine to prevent or delay the emergence of drug resistance in patients treated with a particular drug specific for a microorganism where the drug affects the replication of the microorganism at the conclose protein, which is expected to provide optimal cyclotoxic T lymphocyte (CTL) induced therapeutic protection to the cohort examined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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770 -RDLLIJAARIVELLGRRGWEVLKYWWNLLQYWSQELKSSAVSLLNATAIAVAEGTDRVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphic marker; host response; HIV; AIDS related virus; v
hepatitis related virus; HCV; HBV; drug resistance; envelope.
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84.8%; Pred. No. 5e-205;
ive 45; Mismatches 69;
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                                                                                                                 841 QVLQRVGRALLHIPTRIRQGLERALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus
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The invention relates to a method of identifying a human immunodeficiency virus type-1 (HIV-1) envelope protein which produces a cross-reactive immune response following administration in a mammal by: (a) substituting one or more amino acids in or near the gp41, CD4-binding, co-receptorbinding or outer domains of gp120; and (b) identifying one or more amino acids substitutions in the domains that produce a cross-reactive immune response following administration in a mammal. The method is useful for identifying an HIV-1 envelope protein, which produces a cross-reactive immune response following administration in a mammal. Compositions comprising such HIV-1 envelope protein may be used as HIV subunit vaccine or immunogenic composition that can induce antibodies that neutralize HIV strains across different phenotypes and clades, or for the prevention or therapy of HIV-1 infection. This sequence corresponds to the gp120 envelope glycoprotein from a neutralisation antibody-resistant (primary) mustrain of HIV-1 (MN-P).
                                                                                                                                                                                                                                      Identifying an HIV-1 envelope protein that produces a cross-reactive immune response in a mammal, comprises introducing amino acid substitutions into ap120, and identifying substitutions that produce cross-reactive immune response.
                                                                                                                                                                                                                                                                                                                      Disclosure, SEQ ID NO 2; 68pp; English
                                                                                           10-MAY-2002; 2002US-0379052P.
                                                             12-MAY-2003; 2003WO-US014721
                                                                                                                            (JACK-) JACKSON FOUND HENRY
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N-PSDB; ADP04368.
 WO2004045495-A2
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YDTEAHNVWATHACVPTDPNPQEVELVNVTENFNWWKNNMVEQMHEDIISLWDQSLKRPCV 119
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                61 YDTEVHNVWATHACVPTDPNPQEVVLENVTENVTENFNMWKNNNWVEQMHEDIISLWDQSLKPCV
                                                               KLTPLCVTLNCTDLRNTTNTNNSTDNNNSNSEGTIKGGEMKNCSFNIATSIGDKMQKEYA
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                                                                                                                                                                                                                                                         300 NCSRPNNNTRKSIP--MGPGRAFYTTGQIIGDIRQAHCNISKTNWTNALKQVVEKLGEQF
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                                                                                        MRVKGIRRNYQHWWGWGTWLLGLLMICSATEKLWVTVYYGVPVWKEATTTLFCASDAKAY
                                                                                                                            DTEAHNVWATHACVPTDPNPQEVELVNVTENFNMWKNNMVEQMHED11SLWDQSLKPCVK
                                                                                                                                         DIEVHNVWATHACVPTDPNPQEVQLVNVTEDFNNWKNNMVEQMHEDIISLWDQSLKPCVK
                                                                                                                                                                              LTPLCVTLNCTDLRNTTNTNNST-----DNNNSNSEGTIKGGEMKNCSFNIATSIGDKM
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                                                                         MRVKGIRRNYQHWWGWGTWLLGLLMICSATEKLWVTVYYGVPVWKEATTTLFCASDAKAY
                                                 Gaps
                                                 15;
                      Length 863;
                                                 Indels
                        DB 8;
                                          3;
83;
                     ; Score 3859.5; DE; Pred. No. 5e-203; 47; Mismatches 8
                        83.6%;
              Query Match
Best Local Similarity 83.4%
Sequence 863 AA;
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CD4-binding;

anti-HIV; vaccine; human immunodeficiency virus type-1; envelope glycoprotein; cross-reactive immune response; gp41; co-receptor-binding; outer domain; gp120.

Human immunodeficiency virus 1.

Envelope protein gp120 from antibody resistant HIV strain

(first entry)

26-AUG-2004

ADP04369

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ADP04369 standard; protein;

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532
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                                                                                                                                                                                                                                                                                                                       593 YLRDQQLLGIWGCSGKLICTTTVPWNASWS-NKSQEDIWNNYTWMQWEREIDNYTSTIYE 651
                                                                                                                                                                                                                                                     VNRVRQGYSPLSFQTRLPAPRGPDRPEEIEEEGGDRDRDRSGLLVDGFLTLIWVDLRSLC 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a nucleic acid encoding a modified viral envelope glycoprotein gene of an HIV-1 isolate comprising a nucleotide segment that encodes a modified form of an HIV-1 gpl20 and gp41 complex,
                                                                                                                                                                                                                                                                                                         LFSYHRLRDLLLIVTRIVELLGRRGWEILKYWWNLLQYWSQELKNSAVSLFNATAIAVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene of an HIV-1 isolate,
                                                       474 EIFRPGGGDMRDNWRSELYKYKVVTIEPLGVAPTKAKRRVVQREKRA-AIGALFLGFLGA
                                                                                          535 AGSTMGAASVTLTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWGIXQLQARILAVER
                                                                                                           YLKDQQLLGIWGCSGKLICTTTVPWNASWSKNKTLEAIWNNMTWMQWDKEIDNYTSLIYS
                                                                                                                                                                                                              ETFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREERAVGLGAMFFGFLGA
                                                                                                                                                                                                  LIEESPIQQEKNEQELLELDKWANLWNWFDISNWLWYIKIFIMIVGGLVGLRIVFVVLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A nucleic acid encoding a modified viral env gene of an HIV-1 isolate useful as a vaccine for treating or reducing the severity of a viral disease, e.g. HIV infection, or reducing the likelihood of a subject becoming infected with a virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV; gpl20; gp41; gp160; glycoprotein; AIDS; gp140; variable loop; vaccine; viral disease; HIV infection; cytotoxic T lymphocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olson WC, Maddon PJ,
                                                                                                                                                                                                                                                                                                                                                             998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus 1; isolate JR-FL
                                                                                                                                                                                                                                                                                                                                                                           835 GTDRVIQVLQRVGRALLHIPTRIRQGLERALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ADAR-) ADARC AARON DIAMOND AIDS RES CENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADK14406 standard; protein; 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-2000; 2000US-00602864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0141168P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV wild-type gp160 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neutralising antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-256072/24.
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where the modifications comprise a V35C, Y39C, W44C, P484C, G488C, C759C, C7 W490C, or A492C mutation in gp120 and a D580C, W597C, T596C, C7 W601C mutation in gp11, such mutations being numbered by reference to the gp160 (precursor of gp41 and gp120) HIV-1 isolate JR-FL and the modifications resulting in a disulphide bond between gp120 and the stabilises the otherwise non-covalent gp120-gp41 interaction. The stabilization results in enhanced binding of the disulphide-bonded gp120-gp41 complex to HIV-1 non-neutralising antibodies and reduced binding cf the complex to HIV-1 non-neutralising antibodies and reduced binding cf the complex to HIV-1 non-neutralising antibodies and reduced binding cf the complex to HIV-1 non-neutralising the nucleic acid cited above, a copplicable vector comprising the nucleic acid, a host cell comprising the replicable vector and a composition which comprises the nucleic acid. The modified gp120 is further characterised by the absence of one or more applied and gp10 which has the proteolytic cleavage site between gp120 and gp41 resulting in a 140kDa proteolytic cleavage site between gp120 and gp41 resulting in a 140kDa proteolytic cleavage site between gp120 is further characterised by the absence or prior to ransmembrane domain of gp41 resulting in a 140kDa proteolytic cleavage site between gp120 is further characterised by the absence or prior treating a viral disease, e.g. HIV infection (AIDS).

Credicines for treating a viral disease, e.g. HIV infection of the pilote comprises or enfancing in the severity of a viral disease, org. HIV infection of the control of a subject becoming infected with a virus, the control of the gp120 of a viral disease, org. HIV infection of the dp120 of a viral disease, org. HIV infection of the dp120 of a subject becoming infected with a virus, and the dp120 of a viral disease, org. HIV infection of the dp120 of a virial disease, and the dp120 of a ģ 120 300 405 480 462 522 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCNISKTNWTNALKQVVEKLGEQFNKT 360 9 a subject production of antibodies or cytotoxic T lymphocytes. The present sequence is wild-type HIV gp160 protein. NOTE: This sequence is not shown in the specification but was obtained from genbank reference 61 DIEVHNVWATHACVPTDPNPQEVVLENVTEHFNWWKNNMVEQMQEDIISLWDQSLKPCVK KGSCKNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSENFTNNAKTIIVQLREPVKIN 233 KGPCKNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSDNFTNNAKTIIVQLKESVEIN 406 TLPCRIKQIINNWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGINEN---GTEIFRPG DTEAHNVWATHACVPTDPNPQEVELVNVTENFNWWKNNMVEQMHEDIISLWDQSLKPCVK 181 LYKLDIEPIDNDNTSYRLISCNTSVITQACPKISFEPIPIHYCAPAGFAILKCNDKKFSG 353 IIVFNHSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTWN------NNTEGSNNTEGN-TI GGDMRDIWMRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVGIGAVFLGFLGAAGSTMG 1 MRVKGIRKSYQYLWKGGTLLLGILMICSAVEKLWVTVYYGVPVWKEATTTLFCASDAKAY LTPLCVTLNCTDLRNTTNTNNSTDNNNSNSEGTIKGGEMKNCSFNIATSIGDKMQKEYAL 361 KIVFTNSSGGDPEIVTHSFNCAGEFFYCNTTQLFDSIWNSENGTWNITRGLNNTGRNDTI TLPCRIKQIINRWQEVGKAMYAPPIKGNISCSSNITGLLLTRDGGKDDNSRDGNETFRPG GGDMRDNWRSELYKYKVVKI EPLGVAPTKAKRKVVQREERAVGLGAMFFGFLGAAGSTMG 1 MRVKGIRRNYQHWWGWGTMLLGLLMICSATEKLWVTVYYGVPVWKEATTTLFCASDAKAY Gape 19; 8; Length 847; 65; Indels 83.3%; Score 3845.5; DB 8 84.1%; Pred. No. 2.9e-202; tive 54; Mismatches 65; U63632 (DNA entry, proteins shown). Query Match Best Local Similarity 84.1%, Matches 728; Conservative Sequence 847 AA; 421 301 61 121 241 293 481 463 셤 셤 유 셤 g ઠે g à g ò 엄 8 ò ò ଚ ò 엄 ð

541 AASVTLTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQ

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721 GYSPLSFOTRLPAPRGPDRPERIEBEGGDRDRDRSGLLVDGFLTLIWVDLRSLCLFSYHR 780
                                                         702 GYSPLSFQTLLPAPRGPDRPEGIBEEGGERDRDRSGRLVNGFLALIWVDLRSLCLFSYHR 761
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Search completed: April 11, 2005, 11:08:59 Job time: 295.737 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

April 11, 2005, 10:57:57; Search time 65.6201 Seconds (without alignments) 1269.790 Million cell updates/sec Run on:

1 MRVKGIRRNYQHWWGWGTML......GRALLHIPTRIRQGLERALL 866 US-09-762-261C-1 4617 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	env polyprotein pr	envelope glycoprot	env protein - huma	envelope glycoprot	env polyprotein pr	env polyprotein pr	env polyprotein -	env polyprotein pr		env polyprotein pr	env protein - huma	env polyprotein -	env polyprotein -	env polyprotein pr	env polyprotein pr	env polyprotein pr	envelope polyprote	envelope polyprote	env polyprotein pr	envelope protein p	gag polyprotein -	envelop glycoprote	env polyprotein -	env polyprotein P	env polyprotein M				
SUMMARIES	ID	VCLJMIN	T12016	S13289	T09448	H44001	VCLJSC	VCLJBR	VCLJLV	VCLJH3	VCLJVL	S13288	S33985	VCLJH4	VCLJKB	VCLJ3W	VCLJA2	T01672	S54384	VCLJZR	A44963	VCLJND	VCLJKX	VCLJSI	S49197	A53034	A40218	S31493	62	A41621
	DB	7	~	~	~	-	-	-	Н	-	-	N	N	-4	Н	Н	Н	N	N	Н	Н	Н	Н	-	0	~	~	7	~	N
	Length	859	Ŋ	847	847	843	861	852	861	856	856	854	851	868	861	856	855	859	853	855	856	846	729	854	877	863	206	495	443	445
d	Query Match	86.1	83.6	83.5	83.3	83.2	81.8	81.4	81.3	81.1		80.5	80.4	80.3	80.2	80.1	79.9	76.3	75.8	75.8	73.6	73.6	67.5	59.5	σ	~	47.2	43.0	42.5	42.3
	Score	3977.5	3862	3853.5	3845.5	3839.5	3775.5	3760	3753.5	3744	3731	3716	3710.5	3708	3703.5	3700	3688.5	3523.5	3500.5	3500.5	3398	3396	3117	2746	2300.5	2198	2179	1987.5	1963	1955
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CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCNISKTNWTNALKQVVEKLGEQFNKT 360 361 KIVFTNSSGGDPEIVTHSFNCAGEFFYCNTTQLFDSIWNSENGTWNITRGLNNTGRNDTI 420

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36.2	35.7	35.6 35.4	35.3	34.2	34.2	34.1	34.0	29.6	29.5	29.4	29.5	29.5
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	1661.5 1648.5	1644.5 1636	1629.5	1580.5	1579	1574	1568	1368	1363	1355.5	1349	1348.5

## ALIGNMENTS

174 LEYKLDVVPIDNITTSYRLINCNTSVITQACPKVSFEPIPIHYCTPAGFALLKCKDKKFN 240 GKGSCKNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSENPTNNAKTIIVQLREPVKI 234 GTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSENPTDNAKTIIVQLNESVEI 300 NGSRPNNNTRKSIPMGPGRAFYTTGOIGDIRQAHCNISKTNWTNALKQVVKLLGGGFNK   - - - - - - - - - - - - - - - - - -	QY         480 GGGDMRDNWRSELYKYKVVKIEPIGVAPTKAKRVVQREERAVGLGAMFGFLGGAGSTM 539           LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ein in S PID:9235	Nature 3484, 69-73, 190  A;fitle: HIV-1 tropism for monouclear phagocytes can be determined by regions A;Reference number: S13288; MUID:91043044; PMID:2172833  A;Reference number: S13288; MUID:91043044; PMID:2172833  A;Restaus: preliminary  A;Molecule type: DNA  A;Residues: 1-847 < CORF  A;Residues: 1-847 < CORF  C;Superfamily: type E retrovirus env polyprotein  Cuery Match  Guery Match  Best Local Similarity 84.2%; Pred. No. 3.2e-268;  Matches 729; Conservative 52; Mismatches 66; Indels 19; Gaps 6  Oy  I MRVKGIRRNYQHWWGWGTMLLGLLMICSATEKLWVTVYGVPVWKEATTLFCASDAKAY 60  DD  I MRVKGIRKSYQYLWKWGTMLLGILMICSATEKLWVTVYGVPVWKEATTLFCASDAKAY 60  Oy  G DTEAHNVWATHACVPTDPNPQEVELVNVTENFNWMKNNNVEQWHEBDIISLWDQSLKPCVK 120
	IQQEKNEQELLELDKWANLWNWFDISNWLWYIKIFIMIVGGLNGLRIVFVVLSIVNRVRQ 720	T12016 envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3) C;Species: human immunodeficiency virus type 1, HIV-1 C;Decies: human immunodeficiency virus type 1, HIV-1 C;Decies: lo-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T12016 R;McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H AIDS Res. Hum. Retroviruses 14, 329-337, 1998 A;Attle: Diversity of the human immunodeficiency virus type 1 envelope glycoprof A;Reference number: Z17379; MUID:98178716; PMID:9519894 A;Accession: T12016 A;Accession: T12016 A;Accession: T2016 A;Accession: T2016 A;Accession: T2016 A;Accession: T2016 A;Ccssion: T2016 A;Ccssion: T2016 A;Ccssion: T2016 A;Ccssion: T2016 A;Ccssion: T2016 A;Accession: T20179 A;Accession: T2016 A;Accession: T20171 A;Accession: T2016 A;Accession: T2017 A;Accession: T2017 A;Accession: T2017	Ch 83.6%; Score 3862; DB 2; Length 852;  1 Similarity 84.0%; Pred. No. 8e-269;  228; Conservative 54; Mismatches 69; Indels 16; Gaps 6;  1 MRVKGIRRNYQHWWGTMLLGLIMICSATEKLWVTVYYGVPWKEATTTLFCASDAKAY 60  1 MRVKGIRKNCQHLWKWGTMLLGMLMICSADERLWVTVYYGVPWKEATTTLFCASDAKAY 60  1 MRVKGIRKNCQHLWKWGTMLLGMLMICSADERLWVTVYYGVPWKEATTTLFCASDAKAY 60  61 DTEAHNVWATHACVPTDPNPQEVELVNVTENFNMWKGNHEDIISLWDQSLKPCVK 120  61 DTECHTNVWATHACVPTDPNPQEVLKNVTENFNMWKGNHWZGWHEDIISLWDQSLKPCVK 120  61 DTECHTNVWATHACVPTDPNPQEVLKNVTENFNMWKGNMWZGWHEDIISLWDQSLKPCVK 120  61 DTECHTNVTATTATTNTNNSTDNNSSBGTIKGGEMKNCSFNIATSIGDKMQKEYA 179  62 LTPLCVTLNCTDYLRNDTNTTSNNGGGMEGGEIKNCSFNIATRIGNKVQKEYA 173  80 LLYKLDIEPIDNDNTSYRLISCNTSVITQACPKISPEPIPIHYCAPAGFAILKCNDKKFS 239

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                                                                                                                                                                                                                                                          406 TLPCRIKQFINMMQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGINEN---GTEIFRPG
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                                 173 FYKLDVVPIDNNNTSYRLISCDTSVITQACPKISFEPIPIHYCAPAGFAILKCNDKTFNG
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                                                                                                            KGSCKNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSENFINNAKTIIVQLREPVKIN
                                                                                                                                                                                                                353 TIVENHSSGGDPEIVMHSFNCGGEFFYCNSTQLNNSTWN-----NNTEGSNNTEGN-TI
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envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004
C;Accession: T09448
R;Pang. S;; vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitted to the EMBL Data Library, July 1996

RESULT 4

A, Accession: 19948
A, Status: preliminary: translated from GB/EMBL/DDBJ
A, Solecus: preliminary: translated from GB/EMBL/DDBJ
A, Status: preliminary: translated from GB/EMBL/DDBJ
A, Residues: 1-847 < PAN>
A, Residues: 1-847 < PAN>
A, Cross-references: UNIPROT: Q75760; EMBL: U63632; NID: g1465777; PID: g1465781
C, Genetics:
A, Genetics:
C, Superfamily: type E retrovirus env polyprotein

9 180 480 462 900 582 9 720 780 840 120 120 240 360 352 405 522 641 701 232 9 9 173 FYKLDVVPIDNNNTSYRLISCDTSVITQACPKISFEPIPIHYCAPAGFAILKCNDKTFNG AASVTLTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQ LLGIWGCSGKLICTTVPWNASWSKNKTLEAIWNNWTWMQWDKEIDNYTSLIYSLIEESP 661 IQQEKNEQELLELDKWANLWNWFDISNWLWYIKIFIMIVGGLVGLRIVFVVLSIVNRVRQ DTEAHNVWATHACVPTDPNPQEVELVNVTENFNWWKNNMVEQMHEDIISLWDQSLKPCVK 121 LTPLCVTLNCKDV-NATNTTN-----DSBGTMERGEIKNCSFNITTSIRDEVQKEYAL KGSCKNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSENFTNNAKTIIVQLREPVKIN CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCNISKTNWTNALKQVVBKLGEQFNKT TLPCRIKQIINRWQEVGKAMYAPPIKGNISCSSNITGLLLTRDGGKDDNSRDGNETFRPG GGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQRBERAVGLGAMFFGFLGAAGSTMG LRDLLLIVTRIVELLGRRGWEILKYWWNLLQYWSQELKNSAVSLFNATAIAVAEGTDRVI 353 IIVFNHSSGGDPELVM4SFNCGGEFFYCNSTQLFNSTWN-----NNTEGSNNTEGN-TI LIPLCVILNCTOLRNITNINSTDNNNSNSEGIIKGGEMKNCSFNIAISIGDKMQKEYAL LYKLDIEPIDNDNTSYRLISCNTSVITQACPKISFEPIPIHYCAPAGFAILKCNDKKFSG KIVPTNSSGGDPEIVTHS FNCAGEFFY CNTTQL PDS I WNSENGTWNITRGLNNTGRNDTI MRVKGIRRNYQHWWGWGTMLLGLLMICSATEKLWVTVYYGVPVWKEATTTLFCASDAKAY Gaps 19; Indels 65; ; Score 3845.5; DB 2; Pred. No. 1.2e-267; 54; Mismatches 65; 822 BALQRIYRAILHIPTRIRQGLERALL 847 QVLQRVGRALLHIPTRIRQGLERALL 866 tch 83.3%; al Similarity 84.1%; 728; Conservative 5 Query Match Best Local Similarity Matches 728; Conserv 293 61 61 121 181 241 233 361 406 463 541 523 601 721 702 781 301 421 481 셤 요 ò qq 셤 8 유 ઠે g ઠે 셤 Š g Š g ŝ g 8 8 Š g 8 ò g ठे 셤 ò 8 à

RESULT 5 H44001

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env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)
N;Alternate names: coat polyprotein
A;Alternate names: coat polyprotein
A;Note: host Human immunodeficiency virus type 1, HIV-1
A;Note: host Human immunodeficiency virus type 1, HIV-1
C;Spacies: human immunodeficiency virus type 1, HIV-1
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C;Accession: B28922
A;Accession: B28922
A;Tile: Envelope sequences of two new United States HIV-1 isolates.
A;Reference number: A28922; MUID:88219542; PMID:3369091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protein protein signal sequence #status predicted <SIG>
F;129/comain: signal sequence #status predicted <SIG>
F;30-861/Product: env polyprotein #status predicted <EPP>
F;87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLECRIKEIINMWQEVGKAMYAPPIKGQVKCSSNITGLLLTRDGGNSKNGSKNENTEI 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
        637 QNQQEKNEQELLALDKWASLWNWFDITKWLWYIKIFIMIVGGLIGLRIVFVVLSJVNRVR
                                                           720 QGYSPLSFQTRLPAPRGPDRPEEIEEEGGDRDRDRSGLLVDGFLTLIWVDLRSLCLFSYH
                                                                                         697 QGYSPLSFQTHLPAQRGPDRPDGIEEEGGERDRDRSGPLVDGFLAIIWVDLRSLCLFSYH
                                                                                                                                                                                                              757 RLRDLLLIVTRIVELLGRRGWGVLKYWWNLLQYWIQELKNSAVSLLNATAIAVAEGTDRV
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                                                                                                                                                                780 RLRDLLLIVTRIVELLGRRGWEILKYWWNLLQYWSQELKNSAVSLFNATAIAVAEGTDRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTPLCVTLNCTDLRNTTNTNNSTDNNNSNSEGTIKGGEMKNCSFNIATSIGDKMQKEYAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRVKGIRRNYQHWWGWGTMLLGLLMICSATEKLWVTVYYGVPVWKEATTTLFCASDAKAY
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Pred. No. 1.3e-262;
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Gene: env
;Superfamily: type E retrovirus env polyprotein
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Best Local Similarity 82.3%; Pred. No. 1.3e-
                                                                                                                                                                                                                                                                                                  840 IQVLQRVGRALLHIPTRIRQGLERALL
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A; Residues: 1-861 <GUR>
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Cisuperfamily: type E retrovirus env polyprotein

Cisuperfamily: type E retrovirus env polyprotein; transmembrane protein

Cisywords: coat protein; glycoprotein; polyprotein; transmembrane protein

Fil-29/Domain: signal sequence #status predicted <SIG>

Fil-39/Domain: signal sequence #status predicted <GPI>

Fil-39/Domain: coat protein gp41 #status predicted <GPI>

Figo-489/Product: coat protein gp41 #status predicted <GP2>

Figo-489/Region: hydrophobic

Figo-489/Region: hydrophobic
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                                                   R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M. J. Virtol. 66, 6587-660, 1992. Aftile: Complete nucleotide sequence, genome organization, and biological properties A;Reference number: A44001; MUID:93021387; PMID:1404605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 LTPLCVTLNCTDLRNTTNTNNSTDNNNSNSEGTIKGGEMKNCSFNIATSIGDKMQKEYAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 LYKLDIEPIDNDNTSYRLISCNTSVITQACPKISFEPIPIHYCAPAGFAILKCNDKKFSG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 FYNLDVVPI--DNASYRLISCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNG 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540 GAASVILTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQ 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 GGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREERAVGLGAMFFGFLGAAGSTM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 K-IVFTNSSGGDPEIVTHSFNCAGEFFYCNTTQLFDSIWNSENGTWNITRGLNNTGRNDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              578 QLLGIWGCSGKLICTTTVPWNTSWS-NKSLNEIWDNWTWMKWEREIDNYTHIIYSLIEQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 843;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.2%; Score 3839.5; DB 1. ilarity 84.0%; Pred. No. 3.2e-267; Conservative 46; Mismatches 68;
                                                                                                                                                                                                        Residues: 1.843 <LIY>
Cross-references: UNIPROT:P35961; GB:M93258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                   Molecule type: DNA
                                                                                                                                                             A; Accession: H44001
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C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote F;1-30/Domain: signal sequence #status predicted <SIG> F;31-516/Product: exterior membrane glycoprotein #status predicted <EXT> F;51-516/Product: transmembrane glycoprotein #status predicted <TMM> F;81-141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411, F;616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Riwain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.

Call 140, 9-17, 1985

Gill 140, 9-17, 1985

A;Title: Nucleotide sequence of the AIDS virus, LAV.

A;Reference number: A90866; MUID:85099333; PMID:2981635

A;Accession: A03975

A;Molecule type: DNA

A;Residue type: DNA

A;Residues: 1-861 <WAI>
C;Genetics: UNIPROT:P03377; GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424

C;Genetics:
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                                                                                                                                                                                                       353 KNKTIVFNRSSGGDPEIVMASFNCGGEFFCNTTQLFNSTW-YRNTTGNITEG-----N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 NKTKIVFTNSSGGDPEIVTHSFNCAGEFFYCNTTQLFDSIWNSENGTWNITRGLNNTGRN
                                                                                                                                                                                                                                                                              DTITLPCRIKQIINRWQEVGKAMYAPPIKGNISCSSNITGLLLTRDGGKDDNSRDGNETF
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                                                                                                      KINCSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCNISKTNWTNALKQVVEKLGEQF
                                                                                                                                                                                                                                                                                                                                                                                  RPGGGDMRDNWRSELYKYKVVK1EPLGVAPTKAKRRVVQREERAVGLGAMFFGFLGAAGS
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C,Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change
C,Accession: A03975
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;Superfamily; type E retrovirus env polyprotein;
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NyAlternate names: coat polyprotein
NyAlternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: all-bc-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C;Accession: All667
R;Anand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S;Anand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S;Anand, R.; Thayer, R.; MulD:89085613; PMID:2789516
A;Title: Biological and molecular reharacterization of human immunodeficiency virus (HIV-A;Reference number: A94389; MUID:89085613; PMID:2789516
A;Accession: A31667
A;Accession: A31667
A;Accession: A31667
A;Accession: A31667
A;Accession: A31667
A;Accession: A3167
A;Accession: A31
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                               535
                                                         472 FRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVGTIGAMFLGFLGAA 531
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                                                                                                                                GSTMGAASVTLTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWGIKQLQARILAVERY
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                                                                                     118 PCVKLTPLCVSLKCTDLGNATNT-NSSNTNSSSGEMMEKGEIKNCSFNISTSIRGKVOK
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                                                                                                                                                              1 MRVK---EKYQHLWRWGWKWGTWLLGILMICSATEKLWYTVYYGVPVWKEATTTLFCASD
                                     AKAYDTEAHNVWATHACVPTDPNPQEVELVNVTENFNWWKNNMVEQMHEDIISLWDQSLK
                                                  58 AKAYDTEVHNVWATHACVPTDPNPQEVVLVNVTENFNNWKNDMVEQMHEDIISLWDQSLK
                                                                                                                                                                                                                                           EQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFYCNSTQLFNSTW--FNSTWS-TEGSNN
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                                                                                                                                                                                                                                                                                                           NETFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREERAVGLGAMFFGFLG
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MRVKGIRRNYQH----W-WGWGTMLLGLLMICSATEKLWVTVYYGVPVWKEATTTLFCASD
                                                                                                                                                                                                                                EQFNKTK-IVFTNSSGGDPEIVTHSFNCAGEFFYCNTTQLFDSIWNSENGTWNITRGLNN
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                                                                                                                 EYALLYKLDI EPI DNDNTSYRLI SCNTSVI TQACPKI SFEPI PI HYCAPAGFA I LKCNDK
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A,Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A,Reference number: A93353; MUID:85111123; PMID:2578615
A,Accession: A03973
A,Wolecule type: DNA
A,Residues: 1-856 <RAT>
A,Cross-references: UNIPROT:P03375; GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326: C;Genetics: C; Superfamily: type E retrovirus env polyprotein glycoprotein; immunodeficiency; polyprote (5, Keywords AIDS), capsud protein; ocat protein; ocat protein; signal sequence #status predicted <SIG> F;11-511/Product: exterior membrane glycoprotein #status predicted <EXT> F;22-866/Product: transmembrane glycoprotein #status predicted <TYMN-F;813-136.71-156,160,186.197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict 171 116 58 AKAYDTEVHNVWATHACVPTDPNPQEVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLK 117 236 296 350 413 407 473 464 533 593 643 713 703 773 763 PCVKLTPLCVTLNCTDLRNTTNTNNSTDNNNSNSEGTIKGGEMKNCSFNIATSIGDKMQK 176 231 291 354 524 584 653 CLFSYHRLRDLLLIVTRIVELLGRRGWEILKYWWNLLQYWSQELKNSAVSLFNATAIAVA 833 57 AAGSTMGAASVTLTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWGIKQLQARILAVE SEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVGIGALFLGFLG AKAYDTEAHNVWATHACVPTDPNPQEVELVNVTENFNWWKNNMVEQMHEDIISLWDQSLK PCVKLTPLCVSLKCTDLKNDTNT-----NSSSGRMIMEKGEIKNCSFNISTSIRGKVQK **EYALLYKLDIEPIDNDNTSYRLISCNTSVITQACPKISFEPIPIHYCAPAGFAILKCNDK** KESGKGSCKNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSENFTNNAKTIIVQLREP 232 TFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEBEEVVIRSANFTDNAKTIIVQLNQS VKINCSRPNNNTRKSIPM--GPGRAFYTTGQIIGDIRQAHCNISKTNWTNALKQVVEKLG EQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFYCNSTQLFNSTW--FNSTWS-TKGSNN TGRNDTITLPCRIKQIINRWQEVGKAMYAPPIKGNISCSSNITGLLLTRDGGKDDNSRDG NETFREGGEDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREERAVGLGAMFFGFLG AAGSTMGAASMTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARILAVE RYLKDQQLLGIWGCSGKLICTTTVPWNASWSKNKTLEAIWNNMTWMQWDKEIDNYTSLIY SLIEESPIQQEKNEQELLELDKWANLWNWFDISNWLWYIKIFIMIVGGLVGLRIVFVVLS SLIEESQNQQEKNEQELLELDKWASLWNWFNITNWLWYIKLFIMIVGGLVGLYGLYFAVLS IVNRVROGYSPLSFOTRLPAPRGPDRPEEIEEEGGDRDRBGGLLVDGFLTLIWVDLRSL MRVKGIRRNYQH----W-WGWGTMLLGLLMICSATEKLWVTVYYGVPVWKEATTTLFCASD EQFNKTK-IVFTNSSGGDPEIVTHSFNCAGEFFYCNTTQLFDSIWNSENGTWNITRGLNN Gaps 24; Length 856; Indels 81.1%; Score 3744; DB 1; 82.4%; Pred. No. 2.3e-260; ative 52; Mismatches 78; Conservative al Similarity 719; Conserv A;Gene: env C;Superfamily: 292 57 117 118 177 237 408 465 534 525 594 644 714 704 774 172 297 355 351 414 474 585 654 Query Match Local a ò g ð g 8

	OAROLLSGIVOOO
Qy 834 EGTDRVIQVGRALLHIPTRIRQGLERALL 866 	Db 525 AAGSTWGAASWTLTVQARQLLSGIVQQQNNLLRAIRAQQHLLQLTVWGIKQLQARILAVE 584  Qy 594 RYLKDQQLLGIWGCSGKLICTTTVPWNASWKKNRTLAINNWWTWQWDKEIDNYTSLIY 653
RESULT 10 VCLJUL env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV) N;Alternate names: coat polyprotein N;Alternate names: coat polyprotein C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004 C;Accession: A03974 R;Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J. Nature 313, 450-458, 1985 A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovi	Db 585 RYLKDQQLLGIMGCSGKLICTTAVPWNASWS-NKSLEQIWNNMTWMEWDREINNYTSLIH  Qy 654 SLIEESPIQQEKNEQELLELDKWANLWNWFDISWLWYIKIFIMIVGGLVGLRIVFVVLS
A;Reference number: A93355; MUID:85111157; PMID:2982104 A;Accession: A03974 A;Molecule type: DNA A;Residues: 1-856 eMUE> A;Cross-references: UNIPROT:P03376; GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g3285	DD 764 CLFSYHRIRDLILIVTRIVELIGRRGWEALKYWWNLLQYWSQELKNSAVSLLNATAIAVA 823  Qy 834 EGTDRVIQVLQRVGRALLHIPTRIRQGLERALL 866  DD 824 EGTDRVIEVVQGAYRAIRHIPRRIRQGLERILL 856
A, Gene: env C;Superfamily: type E retrovirus env polyprotein; glycoprotein; immunodeficiency; polyprot C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot F;1-30/Domain: signal sequence #status predicted <sig> F;31-511/Product: exterior membrane glycoprotein #status predicted <ext> F;512-6/Product: transmembrane glycoprotein #status predicted <twm> F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406 F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic</twm></ext></sig>	
Query Match Best Local Similarity 82.1%; Pred. No. 2e-259; Matches 717; Conservative 50; Mismatches 82; Indels 24; Gaps 11;	Nature 348, 95-74, 1590 A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120 c A;Reference number: S13288; MUID:91043044; PMID:2172833 A;Accession: S13288
OY 1 MRVKGIRRNYOHW-WGWGTWLLGILMICSATBKLWVTVYYGVPVWKEATTTLFCASD 56	A;Status: pretiminary A;Wolecule type: DNA A;Residues: 1-854 <obr> A;Residues: 1-854 <obr> A;Cress-references: UNIPROT: Q25582; UNIPROT: Q25502; UNIPROT: O90178; UNIPROT: Q78243; UNIPROT: C.Suberfamily: type E retrovirus env bolyborotein</obr></obr>
CY ST AKAYDTBAHNVWATHACVPTDPNPQEVELVNVTENFNMWKNNNVEQMHEDIISLMDQSLK 116	Query Match  Query Match  Query Similarity 81.9%; Score 3716; DB 2; Length 854;  Best Local Similarity 81.9%; Pred. No. 2.4e-258;  Matches 715; Conservative 51; Mismatches 81; Indels 26; Gaps 12;
QY 117 PCVKLTPLCVTLNCTDLRNTTNTNNSTDNNNSNSEGTIKGGEMKNCSFNIATSIGDKAOK 176	MRVKGIRRNYQHW-WGWGTMLLGLLMICSATEKLWVTVYYGVDVWKEATTTLFCASD 5
QY 177 EYALLYKLDIEPIDNDNTSYRLISCNTSVITQACPKISFEPIPIHYCAPAGFAILKCNDK 236	57 AKAYDTEAHNWATHACVPTDPNPOEVELVNVTENFNMWKNNWVEQMHEDIISLWDQSLK
OY 237 KPSGKGSCKAVSTVQCTHGIRPVVSTQLLLANGSLAEEEVVIRSENFTNNAKTIIVQLREP 296	117 PCVKLTPLCVTLNCTDLRNTTNTNNSTDNNNSNSECTIKGGEMKNCSFNIATSIGDKMQK 118 PCVKLTPLCVSLKCTDLRNTTNTNTNSTDNNNSNSECTIKGGEMKNCSFNIATSIGDKMQK 118 PCVKLTPLCVSLKCTDLRNDTNTNSSSGRMIMEKGEIKNCSFNISTSTRDKVQK
Qy 297 VKINCSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCNISKTNWTNALKQVVEKLG 354	Qy
OY 355 BOPNKTK-IVFTNSSGDPEIVTHSFNCAGEFFYCNTTOLFDSIWNSENGTWNITRGLNN 413	Oy 237 KFSGKGSCKNVSTVQCTHGIRPVVSTQLLLNGSLAEBEVVIRSENFTNNAKTIIVQLREP 296
Qy 414 TGRNDTITLPCRIKQIINRWQEVGKAMYAPPIKGNISCSSNITGLLLTRDGGKDDNSRDG 473  408 TEGSDTITLPCRIKQFINNMQEVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNNNE 464	297 VKINCSRPNNWTRKSIPMGPGRAFYTTGOIIGDIRQAHCNISKTNWTNALKQVVEKLG  - - - - - - - - - - - - - - - - - - -
Qy 474 NETERPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREERAVGLGAMFGFLG 533 :	355 EQFNKTK-IVFTNSSGDPRIVTHSFNCAGEFFYCNTTQLFDSIWNSENGTWNITRGLNN

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qq	349 EQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFYCNSTQLFNSTWFNSTWS-TEGSNN 405	<b>q</b> 0 .	232 TFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLABEEVVIRSVNFTDNAKTIIVQLNTS 291
oy Dp	414 TGRNDTITLPCRIKQIINRWQEVGKAMYAPPIKGNISCSSNITGLLLTRDGGKDDNSRDG 473 	දු පු	297 VKINCSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCNISKTNMTNALKÇVVEKLG 354  :   :         :          :
k q	474 NETFREGGEDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREERAVGLGAMFFGFLG 533 +	δ, d	355 EQFNKTK-IVFTNSSGGDPEIVTHSFNCAGEFYCNTTQLFDSIWNSENGTWNITRGLNN 413
oy Op	534 AAGSTMGAASVTLTVQARQLLSGIVQQQSNILRAIRAQQHLLQLTVWGIKQLQARILAVE 593	oy Oy	414 TGRNDTITLPCRIKQIINBWQEVGKAMYAPPIKGNISCSSNITGLLITRDGGKDDNSRDG 473 
Qy	594 RYLKDQQLLGIWGCSGKLICTTTVPWNASWSKNKTLEAIWNNWTWMQWDKEIDNYTSLIY 653	ò a	474 NETFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRVVQREERAVGLGAMFFGFLG 533 :
oy Op	654 SLIEESPIQQEKNEQELLELDKWANLANNAFDISNALAVIKIFIMIVGGIVGLRIVFVVLS 713	රු සි	534 AAGSTWGAASVTLTVQARQLLSGIVQQSNLIRAIBAQQHLLQLTVWGIKQLQARILAVE 593 
çy Dp	714 IVNRVRQGYSPLSFQTRLPAPRGPDRPFEIEEEGGDRDRDRGGLLUVDGFLTLIWVDLRSL 773	ò a	594 RYLKDQQLLGIWGCSGKLICTTTVPWNASWSKNKTLEAIWNNMTWMQWDKEIDNYTSLIY 653 
QV Dp	774 CLFSYHRLADILLIVTRIVELLGRRGWEILKYWWNLLQYWSQELKNSAVSLFNATAIAVA 833 	& 43	654 SLIEESPIQOEKNEQELLELDKWANLWNWFDISNWLWYIKIFIMIVGGLVGLRIVFVVLS 713
Qy	834 EGTDRVIQVLQRVGRALLHIPTRIRQGIERALL 866	& g	714 IVNRVRQGYSPLSPQTRLPAPRGPDRPEEIEEGGGDRDRDRSGLLVDGFLTLIWVDLRSL 773 :
RESULT 1 S33985 env poly C;Specie C;Date: C;Access	SSULT 12 13985 NV Polyprotein - human immunodeficiency virus type 1 Species: human immunodeficiency virus type 1, HIV-1 Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004 Carlini, F.	8 8 8	774 CLFSYHRLRDLLLIVTRIVELLGRRGWEILKYWWNLLQYWSOELKNSAVSLFNATAIAVA 833 759 CLFSYHRLRDLLLIVTRIVELLGRRGWEALKYWWNLLQYWSOELKNSAVSLLNATAIAVA 818 834 EGTDRVIQVLQRVGRALLHIPTRIRQGLERALL 866 835 EGTDRVIGVVQGAYRALHIPTRIRQGLERALL 851
submitte A,Refere A,Access A,Status A,Molecu A,Residu A,Cross- C,Superf	submitted to the EMBL Data Library, November 1991 A,Reference number: 833979 A,Rocession: 833985 A,Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-851 < CAR> A;Cross-references: UNIPROT:Q78243; EMBL:Z11530; NID:g60192; PIDN:CAA77628.1; PID:g60199 C;Superfamily: type E retrovirus env polyprotein	RESULT 13 VCLJH4 env polyprotein N,Alternate name N,Contains: coat C,Species: human C,Date: 30-Jun-1	VCLJH4 env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451) N.Alternate names: coat polyprotein N.Alternates coat protein gp120; coat protein gp41 C.Species: human immunodeficiency virus type 1, HIV-1 C.Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
Query Best I Matché	Query Match 80.4%; Score 3710.5; DB 2; Length 851; Best Local Similarity 81.7%; Pred. No. 5.9e-258; Matches 713; Conservative 51; Mismatches 80; Indels 29; Gaps 10;	C, Accessi R, Desai, Proc. Nat A, Title:	Jul. C.2552.3 S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, E. L. Acad. Sci. U.S.A. 83, 8380-8384, 1986 Molecular cloning and primary nucleotide sequence analysis of a distinct human in the company of the control
çy G	1 MRVKGIRRNYQHW-WGWGTMLLGLLMICSATEKLMVTVYYGVPVWKEATTTLFCASD 56	A; Accessi A; Molecul A; Residue	TE MINISTER ANTINO MOLDINO VALUE FRILDINA MONTO
S S	57 AKAYDTEAHNWATHACVPTDENPQEVELVNVTENFNWMKNNNVSQMHEDIISLWDQSLK 116	A; Canetic C; Genetic A; Gene: e C; Superfa	ore drawfmamphary . wie to
çy ge	117 PCVKLTPLCVTLNCTDLRNTTNTNNSTDNNNSNSEGTIKGGEMENCSFNIATSIGDEMOK 176	C, AC, WOLD F; 1-521/P F; 522-868 F; 89, 138,	49,365,371,395,405,409,45
ò a	177 EYALLYKLDIEBIDNDNTSYRLISCNTSVITQACPKISFEPIPIHYCAPAGFAILKCNDK 236	Query Ma Best Loc Matches	Match 80.3%; Score 3708; DB 1; Length 868; Local Similarity 80.5%; Pred. No. 9.2e-258; Indels 14; Gaps 7; es 703; Conservative 56; Mismatches 100; Indels 14; Gaps 7;
δ <i>j</i>	237 KFSGKGSCKNVSTVQCTHGIRPVVSTQLLLNGSLAEBEVVIRSENFTNNAKTIIVQLREP 296	č	1 MRVKGIRRNYQHWGWGTMLLGLLMICSATEKLWVTVYYGVPVWKBATTTLFCASDAKAY 60

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A;Gene: env
C;Superfamily: type B retrovirus env polyprotein; transmembrane protein
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
C;Keywords: coat protein; glycoprotein; predicted <SIG>
F;1-33/Bomain: signal sequence #status predicted <SIG>
F;1-33/Bogion: hydrophobic #status predicted <CP1>
F;34-517/Product: coat protein gp120 #status predicted <CP1>
F;34-517/Region: cleavage processing #status predicted <CP2>
F;38-534/Region: hydrophobic #status predicted <CP2>
F;518-534/Region: hydrophobic #status predicted <TM1>
F;712-861/Domain: intracellular #status predicted <IM1>
F;712-861/Domain: intracellular #status predicted <INT>
F;712-861/Domain: hydrophobic #status predicted 
F;33,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,408,414,
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         A;Cross-references: UNIPROT:P31819; GB:S41266; GB:D01206
C;Genetics:
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Matches 704; Conservative
A; Molecule type: mRNA
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                                            LYKLDIEPIDN-----DNTSYRLISCNTSVITQACPKISFEPIPIHYCAPAGFAILKCND
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VQLREPVKINCSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCNISKTNWTNALKQVV

114 9 54

29;

80.2%; Score 3703.5; DB 1; Length 861; 80.2%; Pred. No. 1.9e-257; iive 65; Mismatches 80; Indels 29;

SDAKAYDTEAHNVWATHACVPTDPNPQEVELVNVTENFNMWKNNMVEQMHEDIISLWDQS

LKPCVKLTPLCVTLNCTDLRNTTNTNNSTDNNNSNSEGTIKGGEMKNCSFNIATSIGDKM

QKEYALLYKLDIEPIDND----NTSYRLISCNTSVITQACPKISFEPIPIHYCAPAGFAI

LKCNDKKFSGKGSCKNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSENFTNNAKTII

410

EKLGEQFNKTKIVFTNSSGGDPEIVTHSFNCAGEFFYCNTTQLFDSIWNSENGTWNITRG

465

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407 WNGTG-PENITLPCRIKQIVNNMQEVGRAMYAPPIRGQIRCSSNITGLLLTRDGGNITQNN
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C;Accession: A42995
R;Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated A;Reference number: A42995; MUID:92351552; PMID:1322587
A;Accession: A42995
                                                                                                                                                                                                                                          env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41) N;Alternate names: coat polyprotein N;Contains: coat protein gp120; coat protein gp41 C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Date: 31 Har-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
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us-09-762-261c-1.rpr

Db   464   EEIFRPGGGNWRDNWRSELYKKYVKIEPLGVAPTKAKRRVVOREKRAVGAIGAMFLGFL 523     Qy   533   GAAGSTWGAASVTLTVQARQLLSGIVQQOSNLLRAIEAQOHLLQLTVWGIKQLQARILAV 592		Search completed: April 11, 2005, 11:15:28 Job time : 77.6201 secs										
Db 705 FTVLSIVNRVRQGYSPLSFQTRLPA-RGPDRPEGIEEEGGERDRDRSGPLVDGLLALIWV 763  Qy 769 DLRSLCLFSYHRLRDLLLIVTRIVELLGRRGWEILKYWWNLLQYWSQELKNSAVSLFNAT 828	RESULT 15 VCLD1 VCLD1 VCLD1 VCLD1 VCLD1 VCLD1 VCD1 VCD1 VCD1 VCD1 VCD1 VCD1 VCD1 VC	A/Gene: env C;Superfamily: type E retrovirus env polyprotein C;Seywords: coat protein; alycoprotein; polyprotein; transmembrane protein F;1-29/Domain: signal sequence #status predicted <sig> F;30-501/Product: coat protein gpl20 #status predicted <gp1> F;502-847/Product: coat protein gp41 #status predicted <gp2> F;87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459</gp2></gp1></sig>	Query Match 80.1%; Score 3700; DB 1; Length 856; Best Local Similarity 81.5%; Pred. No. 3.4e-257; Matches 712; Conservative 49; Mismatches 87; Indels 26; Gaps 10;	OY 1 MRVKGIRRNYQHWMGWGTMLLGLLMICSATEKLWYTVYYGVPVWKEATTTLFCASDAKAY 60	OY 61 DTEAHNVMATHACVPTDBNPQEVELVNVTENFNNMVKNNNVBQMHEDIISLWDQSLKPCVK 120	QY 121 LTPLCVTLNCTDLENTTNTNNSTDNNNSNSEGTIKGGEMKNCSFNIATSIGDKMQKEYAL 180	QY 181 LYKLDIEFIDNDNTSYRLISCNTSVITQACPKISFEPIPIHYCAPAGFAILKCND 235	Oy 236 KKFSGKGSCKNVSTVQCTHGIRPVVSTQLLINGSLAEBEVVIRSENFTNNAKTIIVQLRE 295	QY 296 PVKINCSRPNNNT-RKSIPMGPGRAFYTTGQIIGDIRQAHCNISKTNWTNALKQVVFKLG 354  :   :	Qy 355 EQFNKTKIVFTNSSGGDPEIVTHSFNCAGEFFYCHTQLFDSIWNSENGFWNITECLNNT 414	Qy 415 GRN-DITILPCRIKQINRWQEVGKAMYAPPIKGNISCSSNITGLLLTRDGGKDDNSRDG 473	Qy 474 NETEREGEDMRDNWRSELYKYKVVKIEDLGVAPTKAKBRVVQREBRAVG-LGAMFFGFL 532

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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 11, 2005, 10:39:11; Search time 277.268 Seconds (without alignments) 1599.394 Million cell updates/sec Run on:

US-09-762-261C-1 4617 1 MRVKGIRRNYQHWWGWGTML......GRALLHIPTRIRQGLERALL 866 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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SUMMARIES	;	OI	Q9WPZ4	090294	Q6BC02	ENV HV1MN	Q9YULS	090295	090296	Q7SVL6	Q7SVL4	Q7SVL0	Q7SVL7	092763	Q7SVL5	040222	Q03811	Q8Q2X5	021160	Q9LJY9	041883	QBUNX2	092761	Q91JY8	071260	Q9IK01	Q91JY7	Q7SVL2	Q6EG58	Q6EK29	Q91K13	Q6UZ39	Q6BC19
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ď	Query	Match	9.66	86.4	86.3	96.0	96.0	85.9	85.4	85.2	85.1	84.8	84.6	84.4	84.2	84.2	83.8	83.8	83.7	83.7	83.6	83.6	83.6	83.5	83.5	83.5	83.4	83.4	83.3	83.3	83.3	83.3	83.3
	C	Score	4600	3990.5	3986.5	3970	3969.5	3964.5	3941.5	3931.5	3928	3917.5	3905	3896.5	3886	3886	3870.5	3868	3863.5	3862.5	3862	3859.5	3859	3857.5	3856.5	3854	3851.5	3848.5	3848	3848	3847.5	84	3845.5
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                                                                                                                                                                      Gaps
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR00177; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
Transmembrane.
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                                                                                                                                        DB 2; Length
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                                                                                                          861 AA; 97670 MW; 8136732E44445E56 CRC64;
                                                                                                                                     86.4%; Score 3990.5; DB 2,
86.8%; Pred. No. 8.2e-287;
tive 38; Mismatches 67;
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MEDLINE=98362112; PubMed=9696803;

MEDLINE=98362112; PubMed=9696803;

Park E.J., Vajcic L.K., Anand R., Theodore T.S., Quinnan G.V. Jr.;

"Mutations in both agreemed gp41 are responsible for the broad neutralization resistance of variant human immunodeficiency virus type 1 MN to antibodies directed at V3 and non-V3 epitopes.";

J. Virol. 72:7099-7107(1998).

EMBL; AROYS719, AAC33788.1; -.

HSSP; PO5877; 1NJ0.
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 LYKLDIEPIDNDNTSYRLISCNTSVITQACPKISFEPIPIHYCAPAGFAILKCNDKKFSG
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                                                 KGSCKNVSTVQCTHGIRPVVSTQLLLNGSLAEBEVVIRSENFTNNAKTIIVQLREPVKIN
                                                                                                                                                                         KIVFTNSSGGDPEIVTHSFNCAGEFFYCNTTQLFDSIWNSENGTWNITRGLNNTGRNDTI
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Last annotation update)
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NCBI_TaxID=11676;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
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Exterior membrane glycoprotein.
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01-NOV-1988 (Rel. 09, Last seq
25-OCT-2004 (Rel. 45, Last ann
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T "Comprehensive analysis of the cross-clade neutralizing activity of a panel of anti-HV-1 monoclonal antibodies.";

EMBL; AV669737; AAT67509.1; -. Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; AV669737; C.viral envelope; IEA.

R GO; GO:0019031; C.viral envelope; IEA.

R GO; GO:0019031; C.viral molecule activity; IEA.

R InterPro; IPR000378; BIV GP41.

R Pfam; PF00517; GP41; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane.
NON TER 857 857
SEQUENCE 857 AA; 97206 MW; 4ED03F3D85C91205 CRC64;
                                                                                               25-001-2004 (TrEMBLrel. 28, Created)
25-001-2004 (TrEMBLrel. 28, Last sequence update)
25-001-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                   Viruses, Retroid viruses, Retroviridae, Lentivirus
NCBI_TaxID=11676;
                                                             857 AA
                                                           PRT;
                                                                                                                                                                Envelope glycoprotein (Fragment).
                                                                                                                                                                                                      Human immunodeficiency virus 1.
                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                       AASVTLTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQ
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Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E., Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.; Farrellos sequences of two new United States HIV-1 isolates."; Virology 164:511-536(1988).
-i- MISCELLANEOUS: The MN isolate was taken from a pediatric AIDS 01-NOV-1988 (Rel. 09, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Envelope polyprotein Gp160 precursor [Contains: Exterior glycoprotein (GP120); Transmembrane glycoprotein (GP41)]. Human immunodeficiency virus type 1 (MN isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus. VCBI\_TaxID=11696;

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PDB; 1ACY; X-ray; P=306-329.
PDB; 1NES; X-ray; P=306-329.
PDB; 1NIS; NMR; A=309-324.
PDB; 1NJO; NMR; A=309-324.
HIV; M17449; ENV\$M:
HIV; M17449; ENV\$M:
FIND M1749; FIND M174; I.
3D-structure; AIDS; Coat protein; Glycoprotein; Signal; us-09-762-261c-1.rup

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600 592 99 720 711 780

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GYSPLSLQTRPPVPRGPDRPEGIEEEGGERDRDTSGRLVHGFLAIIWVDLRSLFLFSYHH 771
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MEDLINE=98362112; PubMed=9696803;
MEDLINE=98362112; PubMed=9696803;
Park E.J., Vujcic L.K., Anand R., Theodore T.S., Quinnan G.V. Jr.;
"Mutations in both gp120 and gp41 are responsible for the broad neutralization resistance of variant human immunodeficiency virus type in Mn to antibodies directed at V3 and non-V3 epitopes.";
J. Wirol., 72:7099-7107(1998).
EMBL; AF075722; AAC31819-1;
HSSP, P05877; INJO.
                                                                                                                                                                                    661 IQQEKNEQELLELDKWANLWNWFDISNWLWYIKIFIMIVGGLVGLRIVFVVLSIVNRVRQ
                                                LIGFWGCSGKLICTTTVPWNASWS-NKSLDDIWNMTWWWEREIDNYTSLIYSLIYSLEKSQ
                                                                                                                                                                                                TQQEKNEQELLELDKWASLWNWFDITNWLWYIKIFIMIVGGLVGLRIVFAVLSIVNRVRQ
                                    GGDMRDNWRSELYKYKVVKI EPLGVAPTKAKRRVVQREERAVGLGAMFFGFLGAAGSTWG
                                                                                    AASVTLTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQQ
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86.4%; Pred. No. 2.9e-285;
iive 41; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        857 AA; 97095 MW; 922D362E10C60DA8 CRC64;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:ruccural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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86.0%; Score 3970; DB 1;

Best Local Similarity 86.7%; Pred. No. 2.7e-285;

Matches 751; Conservative 36; Mismatches 69;
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Park B.J., Vujcic L.K., Anand R., Theodore T.S., Quinnan G.V. Jr.;
"Mutations in both gp120 and gp41 are responsible for the broad
reutralization resistence of variant human immunodeficiency virus type
I MN to antibodies directed at V3 and non-V3 epitopes.";
J. Virol. 72:7099-7107(1998).

BEBL, AF07520; AAC31817.1; -.

RESEL, AF07520; AAC31817.1; -.

RESEL, AF07520; C:integral to membrane, IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; C:viral envelope; IEA.

RO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR000777; GP120.

RESEL, FF05617; GP120; 1.

RESEL, GP120; 1.

RESEL, GP120; I.S.

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; Pred. No. 6.9e-285;
42; Mismatches 68;
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Matches 747; Conservative
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361 KIVFINSSGGDPEIVTHSFNCAGEFFYCNTTQLFDSIWNSENGTWNITRGLNNTGRNDTI
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EMBL; AY247219; AAP37147.1; -...
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AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
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GO; GO: 0019028; C: viral capsid; IEA.
GO; GO: 0019031; C: viral envelope; IEA.
GO; GO: 0005198; F: structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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MEDLINE=98362112; PubMed=9696803;

MEDLINE=98362112; PubMed=9696803;

Park E.J., Vujcic L.K., Anand R., Theodore T.S., Quinnan G.V. Jr.;

"Mutations in both gp120 and gp41 are responsible for the broad neutralization resistance of variant human immunodeficiency virus type I MN to antibodies directed at V3 and non-V3 epitopes.";

J. Virol. 72:7099-7107(1998).

EMBL, AR075721; AAC31818.1;

HSSP; P05877; 1NJO.
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                                      LRDLLLIVTRIVELLGRRGWEILKYWWNLLQYWSQELKNSAVSLFNATAIAVAEGTDRVI
                                                                  772 LRDLLLIAARIVELLGRRGWEVLKYWWNLLQYWSQELKSSAVSLLNAAAIAVAEGTDRVI
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0051989; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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85.7%; Pred. No. 3.5e-283;
iive 46; Mismatches 69;
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SEQUENCE FROM N.A.
MEDLINE=2268496; PubMed=12743293;
DDI=10.1158-2268496; PubMed=12743293;
BDO=10.1158-2268496; PubMed=12743293;
Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj J. Brown T.M., Salemi M.L., Vandamme A.M., Kalish M.L.,
"U.S. Human immunodeficiency virus type 1 epidemic: date of opopulation history, and characterization of early strains.";
J. Virol. 77:6359-6366(2003).
HSSP: P20871; 1CE4.
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae;
                        NCBI_TaxID=11676;
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                                                                                  DTEAHNVWATHACVPTDPNPQEVELVNVTENFNWKNNMVEQMHEDIISLWDQSLKPCVK
                                                                                                                                                                                               174 FYKLDVVPIDNDNTNTSYRLISCNTSVITQACPKVSFEPIPIHFCAPAGFALLKCNDKKF
                                                                                                                                                                                                                                                SGKGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSDNFTDNAKTIIVQLKEPVE
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                                                                                                                                   LTPLCVTLNCTDLRNTTNTNNSTDNNNSNSEGTIKGGEMKNCSFNIATSIGDKMQKEYAL
                                                                                                                                                                                   LYKLDIEPIDND--NTSYRLISCNTSVITQACPKISFEPIPIHYCAPAGFAILKCNDKKF
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                                   1 MRVKGIRRNYQHWWGWGTMLLGLLMICSATEKLWVTVYYGVPVWKEATTTLFCASDAKAY
              Gaps
            Indels
Local Similarity 85.1%; Pred. No. 1.9e-282; les 739; Conservative 53; Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                          LIPLCVTLNCTDLRNTTNTNNSTDNNNSNSEGTIKGGEMKNCSFNIATSIGDKMQKEYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 LYKLDIEPIDNDN--TSYRLISCNTSVITQACPKISFEPIPIHYCAPAGFAILKCNDKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 INCSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCNISKTNWTNALKQVVEKLGEQFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIKIVFINSSGGDPEIVIHSFNCAGEFFYCNTTQLFDSIWNSENGTWNITRGLNNTGRND
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                                                                                                                                                                                                                                                                                                          Gaps
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR005158; Env GP41.
FinerPro; IPR00516; GP120; I.
Ffam; PF00516; GP120; I.
Ffam; PF00517; GP41; I.
Ffam; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                Length 850;
                                                                                                                                                                                                                                                                                                        63, Indels
                                                                                                                                                                                                                      850 AA; 96583 MW; 62ED5F6AB033D20B CRC64;
                                                                                                                                                                                                                                                              85.1%; Score 3928; DB 2;
85.3%; Pred. No. 3.5e-282;
iive 45; Mismatches 63;
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.3<sup>3</sup>
Matches 740; Conservative
                                                                                                                                                                                                    Pransmembrane.
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Last sequence update) Last annotation update)

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25, 25, 26,

01-0CT-2003 (TrEMBLrel. 2: 01-0CT-2003 (TrEMBLrel. 2: 01-MAR-2004 (TrEMBLrel. 2: Envelope glycoprotein.

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PRELIMINARY;

Q7SVL4 Q7SVL4;

Q7SVL4 ID Q7 AC Q7 DT Q1 DT Q1 DE ER

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648 SQNQQEKNEQELLELDKWANLWTWFDITNWLWYIKIFIMIVGGLIGLRIVFTVLSIVNRV
                                                                                                                                                                                          356 KTIVFNQSSGGDPEIVTHSFNCGGEFFYCNTTQLFNSTW-----TWNGTBGLNNTBGN--
                                                                                                                                                                                                                                                                                                                                      479 PGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREERAVGLGAMFFGFLGAAGST
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                                                                                 300 NCSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHCNISKTNWTNALKQVVEKLGEQFNK
                                                                                                                                                                    360 TKIVFTNSSGGDPEIVTHSFNCAGEFFYCNTTQLFDSIWNSENGTWNITRGLNNTGRNDT
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                                                                                                                                                                                                                                                                             409 ITLPCRIKQIVNMMQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGNNENGTENGTEIFR
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GKGSCKNVSTVOCTHGIRPVVSTOLLLNGSLAEEEVVIRSENFTNNAKTIIVOLREPVKI
                     236 GKGSCTNVSTVQCTHGIRPVVSTQLLLLNGSLAEEEVVIRSENFTNNAKTIIVQLNESVVI
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SEQUENCE FROM N.A.
MEDIANE-22628496; PubMed=12743293;
DOI=10.1128/JVI.77.11.6359-6366.2003;
DOI=10.1128/JVI.77.11.6359-6366.2003;
Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A.S.,
Brown T.W., Salemi M., Vandamme A.M., Kalish M.L.,
"U.S. Human immunodeficiency virus type 1 epidemic: date of origin,
population history, and characterization of early strains.";
J. Virol. 77:6359-6366[2003).
BRBL; AZ47218; AAP37146.1; --
HSSP; P20871; 1CE4.
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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01-MAR-2004 (TrEMBLrel.
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                                           SQNQQEKNEQELLELDKWASLWNWFDITKWLWYIKIFIMIVGGLVGLRIVFAVLSIVNRV
                     SPIQQEKNEQELLELDKWANLWNWFDISNWLWYIKIFIMIVGGLVGLRIVFVVLSIVNRV
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                                                                                                                            RQGYSPLSFQTRLPAPRGPDRPEGIEEEGGGERDRDRSGRLVDGFLALFWVDLRSLCLFSY
                                                                                                      RQGYSPLSFQTRLPAPRGPDRPEEIEEEGGDRDRDRSGLLVDGFLTLIWVDLRSLCLFSY
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MEDLINE=22658496; PubMed=12743293;
DOI=10.11284/VII.7.11.6359-6366.2003;
MEDLINE=10.11284/VII.7.11.6359-6366.2003;
MEDDIN K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A.S.,
Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;
"U.S. Human immunodeficiency virus type 1 epidemic: date of origin,
population history, and characterization of early strains.";
D. Virol. 77:6359-6366(2003).
EMBL; AX247225; AAP37153.1; -.
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G0; G0:0016021; Cintegral to membrane; IEA.
G0; G0:0019028; C:viral capsid; IEA.
G0; G0:0019031; C:viral envelope; IEA.
G0; G0:0019198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676;
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Pfam; PF00517; GP41; 1.
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                                                            Coat protein; Envelope protein; Glycoprotein; Polyprotein;
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                                                                                                                                               Length 860;
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                                                                                                       860 AA; 97762 MW; A7E185F2BD421590 CRC64
                                                                                                                                           84.6%; Score 3905; DB 2;
84.2%; Pred. No. 1.8e-280;
iive 54; Mismatches 66;
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                                                                                                                                             Query Match
Best Local Similarity 84.2%; Pred. No. 1.8e
Matches 734; Conservative 54; Mismatches
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Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
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EMBL; AFO25755; AAC40592.1; -. HSSP; P04578; 1DLB.
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GO; GO:0019021; C:viral capsid; IEA.
GO; GO:0019021; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR00077; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
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McCutchan F.E., Sanders-Buell E., Salminen M.O., Carr
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Martin M.A., Peden K.W.;
"Construction and characterization of a stable full-length macrophage-
tropic HIV type 1 molecular clone that directs the production of high
titers of progeny virions.";
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                                                            LYKLDIEPIDNDNTSYRLISCNTSVITQACPKISFEPIPIHYCAPAGFAILKCNDKKFSG
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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                                                                                                 LVDQQLLGIWGCSGKLICTTAVPWNASWS-NKSFKEIWNNWTWMEWEKEINNYTRLIYTL
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   GSTMGAASVTLTVQARQLLSGIVQQQSNLLRAIBAQQHLLQLTVWGIKQLQARILAVERY
                         534 GSTMGAASITLIVQARQLLSGIVQQQNNLLRAIEAQQHLLQLIVWGIKQLQARVLAVERY
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MEDLINE=2262496; PubMed=12743293;
MEDLINE=2262496; PubMed=12743293;
BDOI=10.1128/JVI.7.11.6359-6366.2003;
Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A.S.,
Brown T.W., Salemi M., Vandamme A.M., Kalish M.L.,
"U.S. Human immunodeficiency virus type 1 epidemic: date of origin,
population history, and characterization of early strains.";
J. Virol. 77:6359-6366(2003).
EMBL, AY247220; AAP37148.1; --
HSSP; P04578; 1DLB.
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AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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84.2%; Score 3886; DB 2;
Best Local Similarity 84.6%; Pred. No. 4.5e-279;
Matches 733; Conservative 50; Mismatches 69;
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Pfam; PF00517; GP41; 1.
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                              HRLRDLLLIVTRIVELLGRRGWEILKYWWNLLQYWSQELKNSAVSLFNATAIAVAEGTDR
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MEDILINE-91195299; PubMed=2014229;

Mestervelt P., Gendelman H.E., Ratner L.;

Mestication of a determinant within the human immunodeficiency virus 1 surface envelope glycoprotein critical for productive infection of primary monocytes."; proc. netl. Acad. Sci. U.S.A. 88:3097-3101(1991).

EMBL; M60472; AAA45065.1; --

HSSP; P20871; 1CE4.
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0051989; F:structural molecule activity; IEA.
InterPro; IPR000377; GP120.
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Pfam; PF00517; GP41; 1.
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                                                                                                                                                                                                                                                                                                           Length 854;
                                                            Theodore T.S., Englund G., Buckler-White A., Buckler C.E. Martin M.A., Peden K.W.C.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR011010; DNA brk join_enz.
InterPro; IPR000328; Env_GP41.
Pfan: PF0515; GP120;
Pfam; PF0515; GP120;
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84.3%; Pred. No. 4.5e-279;
ive 47; Mismatches 73;
AIDS Res. Hum. Retroviruses 12:191-194(1996)
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352 KTIVFNQSSGGDPEIVWHSFNCGGEFFYCNSTQLFNSTWNF-NGTWNLTQS-NGTEGNDT 409
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HIV-1 gpî HIV-1 V3 Peptide o Antigenic

Scoring table:

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Sequence:

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HIV-1 com HIV-1 Ba-HIV-1 JR-Novel ant

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This sequence represents a human immunodeficiency virus type 1 (HIV-1) R2 strain envelope (env) protein V3 region peptide sequence. The invention relates to the HIV-1 env protein or its fragments, which when administered to a mammal, induces the production of broadly cross-reactive neutralising anti-serum against multiple strains of HIV-1. The HIV-1 env protein and its fragments are useful as vaccines, immunogenic compositions or diagnostic reagents. They can also be used to detect anti-HIV-1/HIV-1 neutralizing antibodies in a sample. The amino acid sequence and its fragments or maNA sequence are useful for generating antibodies in a mammal. In addition, a recombinant delivery vector containing the env amino acid sequence may also be used as a vaccine. (Updated on 12-SBE -2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aav84056 H
Aav84056 H
Aav63735 H
Adr58145 N
                                                          Aar20851
Aar20882
Aar20882
Aar68030
Aar66731
Aaw07390
Aaw07390
Aaw39914
Aaw39014
Aaw
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                                                          AAR20851
AAR20882
AAR20882
AAR68030
AAR68030
AAW03360
AAW31911
AAR318961
AAB71933
AAB71933
AAR41065
AAW41065
AAW43736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY79023 standard; protein; 35 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JACK-) JACKSON FOUND HENRY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US017596
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(first entry)
   \begin{smallmatrix} \mathbf{4} \\ \mathbf{4} \\ \mathbf{5} \\ \mathbf{5} \\ \mathbf{6} \\ \mathbf{5} \\ \mathbf{6} 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-205578/18.
WO200007631-A1
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05-JUN-2000
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   PND EE378
PND EE69
PND EE322
PND EE228
PND EE233
PND EE533
PND EE533
PND EE533
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PND EE665
PND EE665
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Group II
HIV-1 180
HIV-1 V3-
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Aay79020 HIV-1 env
Aar20883 PND EE378
Aar20853 PND EE378
Aar201134 PND EE228
Aar20311 PND EE533
Aar20312 PND EE533
Aar20312 PND EE533
Aar20313 Group II
Aab69350 HIV-1 non
Aar20945 PND EE655
Aar20947 PND EE665
Aar20947 PND EE665
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HIV-1 non
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                                                                                                                                                                                                                April 11, 2005, 10:37:31; Search time 11.4674 Seconds (without alignments) 1180.438 Million cell updates/sec
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Aar29117 (
Aab10703 I
Abg73683 I
Adr50170 I
Adr58150 I
Aar20881 I
Aar21092 E
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                             5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                         1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2105692 segs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                        - protein search, using sw model
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AAR21135
AAR20912
AAR20910
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AAR29113
AAB69350
AAR20945
AAR20946
AAR29110
AAR29110
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AAR20953
AAR20853
AAR21134
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AAR21092
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Gapop 10.0 , Gapext 0.5
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geneseqp2000s:*
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geneseqp2001s:*
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geneseqp2003s:*
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length: 2000000000
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Match Length DB
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RESULT 2

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The sequences represented in AAQ21054-61, AAQ21194-311 and AAQ21321-78 encode PNDs of HIV (envelope protein) which are useful as immunogens for ALDS vaccines, partic. in the form of conjugates. To prepare antigenic conjugates, PND (of HIV) and Omp (of Neisseria) are prepar separately, then linked by cross-linking agents, monogeneric spacers or bigeneric spacers. The conjugate may comprise 1-50 PNDs. A PND has 35 amino acids or less, but at least 5, it contains Gly-X-Gly, where X is Pro, Leu, Ala Gln or Ser. The conjugates as AIDS or HIV vaccines can be used pre- or post- exposure to prevent or treat HIV infection or disease, and are capable of producing an immune response specific for the immunogen. See also AAQ21052-61, AAQ21194-311 and AAQ21321-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         covalently linked to outer membrane proteosome of Neisseria, useful as vaccine and in treating and preventing HIV infections, AIDS and ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antigenic conjugate of HIV major neutralisation determinant
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                                                                                                                                                                                           HIV; PND; principal neutralising determinant; Omp; Neisseria; outer membrane proteosome; AIDS; vaccine; envelope gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 185; DB 2; Length 35; Pred. No. 2.5e-17; 3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 175 + 117-118; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 94.9%; Score 185; DE Simijarity 91.4%; Pred, No. 2.5e 32; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterbury JA;
                      AAR20883 standard; protein; 35 AA.
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90US-00566656.
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Best Local Simijarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR20953 standard;
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                                                                                                                                                                                                                                                                                                                                                                                         07-AUG-1991;
                                                                                                           01-JUN-1992
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                                                                AAR20883;
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AAR20953
ID AAR2
ID AAR2
XX AC AAR2
XX
DT 01-J
XX
DE PND
XX
KW HIV;
KW OUTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a human immunodeficiency virus type 1 (HIV-1) envelope (env) protein amino acid sequence. The invention relates to the HIV-1 env protein or its fragments, which when administered to a mammal, induces the production of broadly cross-reactive neutralising anti-serum against multiple strains of HIV-1. The HIV-1 env protein and its reagents are useful as vaccines, immunogenic compositions or diagnostic reagents. They can also be used to detect anti-HIV-1/HIV-1 neutralizing antibodies in a sample. The amino acid sequence and its fragments or mRNA sequence are useful for generating antibodies in a mammal, In addition, a recombinant delivery vector contening the env amino acid sequence may also be used as a vaccine. (Updated on 12-SEP-2003 to standardise OS
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                                                                                                           Gaps
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0
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                                                          100.0%; Score 195; DB 3; Length 35; 100.0%; Pred. No. 1.1e-18; ive 0; Mismatches 0; Indel8
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                                                                                                                                                     1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV-1 envelope protein amino acid sequence.
                                                                                                                                                                                                                                                                                                      AAY79020 standard; protein; 866 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 33; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus 1.
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                                                                100.08;
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                                                                                                           Conservative
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                                                                                  Local Similarity
tes 35; Conserv
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                      Sequence 35 AA;
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05-JUN-2000
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Gaps

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RESULT 3

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The sequences represented in AAQ21054-61, AAQ21194-311 and AAQ21321-78 encode PNDs of HIV (envelope protein) which are useful as immunogens for AIDS vaccines, partic. in the form of conjugates. To prepare antigenic conjugates, PND (of HIV) and Omp (of Neisseria) are prepd. separately, then linked by cross-linking agents, monogeneric spacers or bigeneric spacers. The conjugate may comprise 1.50 PNDs. A PND has 35 amino acids or less, but at least 5, it contains Gly-X-Gly, where X is Pro, Leu, Ala, Gln or Ser. The conjugates as AIDS or HIV vaccines can be used pre- or peach or prevent or treat HIV infection or disease, and are capable of producing an immune response specific for the immunogen. See also AAQ21052-61, AAQ21194-311 and AAQ21321-78
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                                                                                                                                         New antigenic conjugate of HIV major neutralisation determinant - covalently linked to outer membrane proteosome of Neisseria, useful vaccine and in treating and preventing HIV infections, AIDS and ARC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSRPNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 175 + 93-94; 177pp; English
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                                        Waterbury JA;
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90US-00566654.
90US-00566656.
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nes 32, Conservative
(MERI ) MERCK & CO INC
                                          Lewis JA, Davide JP,
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N-PSDB; AAQ21232.
                                                                                                    N-PSDB; AAQ21268
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Human immunodeficiency virus.
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            The sequences represented in AAQ21054-61, AAQ21194-311 and AAQ21321-78 encode PNDs of HIV (envelope protein) which are useful as immunogens for AIDS vaccines, partic. in the form of conjugates. To prepare antigenic conjugates, PND (of HIV) and OMP (of Neisseria) are prepd. separately, then linked by cross-linking agents, monogeneric spacers or bigeneric spacers. The conjugate may comprise 1-50 PNDs. A PND has 35 amino acids or less, but at least 5, it contains Gly-X-Gly, where X is Pro, Leu, Ala, Gln or Ser. The conjugates as AIDS or HIV vaccines can be used pre- or personne to prevent or treat HIV infection or disease, and are capable of producing an immune response specific for the immunogen. See also AAQ21052-61, AAQ21194-311 and AAQ21321-78
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93.8%; Score 183; DB 2; L.
Best Local Similarity 91.4%; Pred. No. 4.6e-17;
Matches 32; Conservative 2; Mismatches 1;
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covalently linked to outer membrane proteosome of Neisseria, useful as
vaccine and in treating and preventing HIV infections, AIDS and ARC.
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 93.8%; Score 183; DB 2;
91.4%; Pred. No. 4.6e-17;
iive 2; Mismatches 1
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Pred. No. 4.6e-17;
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93.8%; Score 183; DE
Best Local Similarity 91.4%; Pred. No. 4.6e
Matches 32; Conservative 2; Mismatches
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                                32; Conservative
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Query Match
Best Local Similarity
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AAR20912;

RESULT 9

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The sequences represented in AAQ21054-61, AAQ21194-311 and AAQ21321-78 encode PNDs of HIV (envelope protein) which are useful as immunogens for AIDS vaccines, partic. in the form of conjugates. To prepare antigenic conjugates, PND (of HIV) and OMP (of Neisseria) are prepd. separately, then linked by cross-linking agents, monogeneric spacers or bigeneric spacers. The conjugate may comprise 1-50 PNDs. A PND has 35 amino acids or less, but at least 5, it contains Gly-X-Gly, where X is Pro, Leu, Ala, Gln or Ser. The conjugates as AIDS or HIV vaccines can be used pre- or payener to prevent or treat HIV infection or disease, and are capable of producing an immune response specific for the immunogen. See also AAQ21052-61, AAQ21194-311 and AAQ21321-78
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covalently linked to outer membrane proteosome of Neisseria, useful as
vaccine and in treating and preventing HIV infections, AIDS and ARC.
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outer membrane proteosome; AIDS; vaccine; envelope gene.
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                                                                                                                                                                                                                                                         (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                Lewis JA, Davide JP,
                                                                                                                                                                                                                                                                                                                                        WPI; 1992-058471/08
                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ21334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35 AA;
                                                                                                                                     07-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1992
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                                                                                                                                                                          13-AUG-1990;
                                                                                                                                                                                                   13-AUG-1990;
                                                                                                                                                                                                                    13-AUG-1990;
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                                                                                               19-FEB-1992
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                                                        EP471407-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antigenic conjugate of HIV major neutralisation determinant - covalently linked to outer membrane proteosome of Neisseria, useful as vaccine and in treating and preventing HIV infections, AIDS and ARC.
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                                                                                                                                                                                               HIV; PND; principal neutralising determinant; Omp; Neisseria; outer membrane proteosome; AIDS; vaccine; envelope gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.8%; Score 183; DB 2; 91.4%; Pred. No. 4.6e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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                                     AAR20912 standard; protein; 35 AA.
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                                                                                                                                                                                                                                                           Human immunodeficiency virus
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Best Local Similarity 91.4
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MERI ) MERCK & CO INC.
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                                                                                                                                                                                                                                                                                                                                                                               07-AUG-1991;
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AAR20910;

RESULT 10

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**AAR20910** 

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Principle neutralising determinant peptide(s) of HIV gp120 protein - used for diagnosing, preventing and treating HIV infection.
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                                                                 Example 1; Page 10; 26pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 1.
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           WPI; 1992-400517/49.
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                                                                                                                                                                                                                                                                 correct PN field.)
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20-APR-2001
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                                                                                                                                                     The sequences represented in AAQ21054-61, AAQ21194-311 and AAQ21321-78 encode PNDs of HIV (envelope protein) which are useful as immunogens for ADGS vaccines, partic. in the form of conjugates. To prepare antigenic conjugates, PND (of HIV) and OMP (of Neisseria) are prepd. separately, then linked by cross-linking agents, monogeneric spacers or bigeneric or less, but at least 5, it contains Gly-X-Gly, where X is Pro, Leu, Ala, Gln or Ser. The conjugates as AIDS or HIV vaccines can be used pre- or pass-to prevent or treat HIV infection or disease, and are capable of producing an immune response specific for the immunogen. See also AAQ21052-61, AAQ21194-311 and AAQ21321-78
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/note= "classification of PND peptides is determined by
the predicted secondary structure of this region - see
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                        New antigenic conjugate of HIV major neutralisation determinant -covalently linked to outer membrane proteosome of Neisseria, useful vaccine and in treating and preventing HIV infections, AIDS and ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Principal Neutralising determinant; Human immunodeficiency virus; vaccine; Robson's analytical method; polymerase chain reaction; Garnier-Osguthorpe-Robson method; GOR method; secondary structure.
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                                                                                                                                                                                                                                                                                                                        93.8%; Score 183; DB 2; Length 35; 91.4%; Pred. No. 4.6e-17; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                   1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comments"
15. 18
/note= "conserved PND motif"
                                                                                                                                    Claim 1; Page 175 + 66; 177pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KAGA ) CHEMO SERO THERAPEUTIC RES INS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Group II HIV gp120 PND peptide 8926C.
                                 Waterbury JA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR29113 standard; protein; 35 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91JP-00129224
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(first entry)
                                                                                                                                                                                                                                                                                                                                               32; Conservative
          (MERI ) MERCK & CO INC.
                                 Lewis JA, Davide JP,
                                                       WPI; 1992-058471/08.
N-PSDB; AAQ21234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shiosaki K,
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 32, Conserv
                                                                                                                                                                                                                                                                                                    Sequence 35 AA;
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02-APR-1993
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AAR29113
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DNA encoding HIV PND peptides was PCR amplified using genomic DNA from HIV-infected peripheral blood monouncleic cells as template. The amplified fragments were fused to beta-galactosidase coding sequence.

E.coli transformants were cultured to produce the fusion protein. The expressed PND proteins were divided into groups based on their reactivity with neutralising antibodies and their amino acid sequence. The amino acid sequence was analysed using Robson's analytical program for protein secondary structure. Five groups were included in 3 main groups (i.e. groups I, II and III). Group II PND peptides are those which have the structure and X = turn or coil structure). Vaccine preparations strand structure and X = turn or coil structure). Vaccine preparations to develop vaccines able to recognise any HIV variant. See AAQ31607- (231608, AAR28995-R29000 and AAR29110-R29128. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV-1; human immunodeficiency virus; non-subtype B; gag; pol; env; vpu; vif; vpr; tat; rev; nef; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                    virus.
                                         HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antigenic conjugate of HIV major neutralisation determinant - covalently linked to outer membrane proteosome of Neisseria, useful as vaccine and in treating and preventing HIV infections, AIDS and ARC.
                                                                                                                                                    Gaps
number of human immunodeficiency virus (HIV) type 1 non-subtype B isolates. The sequences shown include the near full-length coding sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, rev and nef proteins. These can be used to detect the presence of H in a sample and to produce antibodies against non-subtype B HIV-1 v These antibodies can be used in vaccines to prevent and treat HIV infection. (Updated on 12-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                  determinant; Omp; Neisseria;
vaccine; envelope gene.
                                                                                                                           Length 842;
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                                                                                                                         Score 181; DB 3; I
Pred. No. 2.2e-15;
4; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterbury JA;
                                                                                                                                                                                                                                                                                                                                                                  HIV; PND; principal neutralising outer membrane proteosome; AIDS;
                                                                                                                                                                                                                                                                AAR20945 standard; protein; 35
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90US-00566654.
90US-00566656.
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                                                                                                                          Query Match
Best Local Similarity 88.6%;
Matches 31; Conservative
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                                                                                                    Sequence 842 AA;
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13-AUG-1990;
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92.3%; 88.6%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV; PND; principal neutralising determinant; Omp; Neisseria;
outer membrane proteosome; AIDS; vaccine; envelope gene.
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35
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                                 1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 175 + 163; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: April 11, 2005, 11:09:03 Job time : 12.4674 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lewis JA, Davide JP, Waterbury JA;
                                                                                                                                                                                                      Ą.
                                                                                                                                                                                                      AAR20947 standard; protein; 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-00566638.
90US-00566654.
90US-00566656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91EP-00202025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-058471/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ21364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                     01-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1990;
13-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                              PND EE665-3.
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                                                                                                                                                                                                                                                            AAR20947;
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                                                                                                                                                                           AAR20947
                                                                                                                                          RESULT
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                 Copyright
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OM protein - protein search, using sw model

April 11, 2005, 10:57:57; Search time 2.65208 Seconds (without alignments) 1269.790 Million cell updates/sec Run on:

US-09-762-261C-3 195 1 CSRPNNWTRKSIPMGPGRAFYTTGQIIGDIRQAHC 35 Title: Perfect score: Sequence:

Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		<b>æ</b> (				
Result No.	Score	Watch	Length	DB	ID	Description
	180	92.3	35	7	PC2296	V3 domain peptide
7	176	。	35	7	m	n pept
٣	176	90.3	77	~	S35862	velope p
4	176	0	110		A46410	
ß	176	•	847		T09448	
9	176	90.3	847		S13289	a)
7	175	σ	16	7	835859	
80	175	89.7	77	7	S35820	
6	175	89.7	77	7	S35819	
. 10	174	89.3	443	~	162	Q.
11	173	88.7	77	7	S35834	envelope protein -
12	173	88.7	77	7	583	
13	173	88.7	77	ď	835835	
14	172	88.2	77	ď	S35848	
15	172	88.2	77	N	S35849	
16	172	88.2	77	~	835857	124
17	171	87.7	35	7	PC2297	•
18	171	87.7	46	7	G01847	ц
19	171	87.7	77	7	S35823	
20	171	87.7	77	7	835809	
21	171	87.7	110	~	B46410	envelope protein (
22	171	87.7	110	7	C46410	envelope protein (
23	171	87.7	290	7	S25940	env protein - huma
24	171	87.7	445	0	A41621	env polyprotein M
25	170	•	77	7	ß	
26	170	7.	77	~	S35841	
27	170	87.2	77	~	35	envelope protein -
	170	٠	77	~	358	
	170	87.2	77	~	S35850	envelope protein -

C; Accession: PC2295
R; Sherefa, K.; Soennerborg, A.; Steinbergs, J.; Saellberg, M.
Biochem. Biophys. Res. Commun. 205, 1658-1664, 1994
A; Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotyping ar A; Reference number: PC2291; MUID:95110306; PMID:7811250
A; Accession: PC2295
A; Accession: PC2295
A; Residues: 1-35 < SHE>
A; Residues: 1-35 < SHE>
A; Cross-references: UNIPROT:Q8JA81; UNIPROT:Q8JA72; UNIPROT:Q8JA67; UNIPROT:Q8JA75; UNIPROT:Q8JA67; UNIPROT:Q8JA75; UNIPROT:Q8JA81; UNIPROT:Q8JA75; U

PC2295
V3 domain peptide P4317 - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 21-Feb-1995 #sequence\_révision 05-Apr-1995 #text\_change 09-Jul-2004

RESULT 2

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1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC 35

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Gaps

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Query Match 90.3%; Score 176; DB 2; Length 35; Best Local Similarity 88.6%; Pred. No. 8e-18; Matches 31; Conservative 3; Mismatches 1; Indels

RESULT 3 S35862

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1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC 35

H44001 env polyprotein pr	S42918 env polyprotein -	S35821 envelope protein -	S35824 envelope protein -				S42904 env polyprotein -	S42905 env polyprotein -	S42898 env polyprotein -	S35815 envelope protein -		S35800 envelope protein -		S60529 envelope polyprote	VCLJA2 env polyprotein pr	ALIGNMENTS  RESULT 1  PC2296  V3 domain peptide P4346 - human immunodeficiency virus type 1 (fragment) C;bpciese human immunodeficiency virus type 1, HIV-1 C;Date: 21-Peb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004 C;Accession: PC2296	R;Sherefa, K.; Soennerborg, A.; Steinbergs, J.; Saellberg, M.	Blochem, Blophys. Kes. Commun. 209, 1658-1664, 1994 A,Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotypir A. Deference number. PC2941. MITD. 95110306. PMTD.7811750
H44	842	83	83	83	046	Ş	S42	847	\$42	33	A4(	83	33	36	ΛCI	immi Y vi Visi	Ste	05, 1nf
7	7	~	N	~	~	٦	7	~	~	~	7	~	7	~	Т	nan Lenc	' . نـ	7. V-1. (UID)
843	7.1	77	77	77	110	852	71	71	71	77	206	77	77	299	855	6 - hum odefici	borg, 1	Communing of HI
87.2	86.7	86.7	86.2	86.2	86.2	86.2	85.6	85.6	85.6	85.6	85.1	84.6	84.6	84.6	84.6	de P434 n immun 1995 #8	Scenner	s. kes. groupin ger: PC
170	169	169	168	168	168	168	167	167	167	167	166	165	165	165	165	n peptic 3: human 21-Feb-1	1, K.;	Blopny Rapid (
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	RESULT 1 PC2296 Cy domain peptide P C'Species: human im C'Date: 21-Feb-1995 C'Accession: PC2296	R;Sherefa	Blochem. A;Title: A:Referen

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Gaps

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Length 35; Indels

Query Match 92.3%; Score 180; DB 2; Best Local Similarity 91.4%; Pred. No. 2.2e-18; Matches 32; Conservative 2; Mismatches 1

A.Accession: PC2266
A.Molecule type: protein
A.Residues: 1-35 < SHE>
A.Cross-references: UNIPROT: Q70826; UNIPROT: Q70831
C.Superfamily: type E retrovirus env polyprotein

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A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
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                                                                               ch 90.3%;
.1 Similarity 88.6%;
31; Conservative
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                                                                                 Query Match
Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-76 <CHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S13289
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                                                                                                                                                                                                                                                                                        ;Cross-references: UNIPROT:077544; UNIPROT:077542; UNIPROT:077545; EMBL:223246; NID:g31
;Experimental source: strain CSF2951 clone3; strain CSF2951 clone4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crieflope protein (V3 domain) - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A6410
R;Accession: A6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Uul-1999 #sequence_revision 16-Uul-1999 #text_change 09-Uul-2004
C;Accession: T09448
R;Pang, S:; Vinters, H:V:; Akashi, T:; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitted to the EMBL Data Library, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z23244; NID:g313631; PIDN:CAA80762.1; PID:g313632; EMBL:Z23247; A;Experimental source: strain CSF2951 clone11; strain CSF2951 clone4
C;Superfamily: type E retrovirus env polyprotein
protein - human immunodeficiency virus type 1 (strain CSF2951) (fragment) 8: human immunodeficiency virus type 1, HIV-1
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;Molecule type: DNA
;Residues: 1-847 <PAN>
;Cross-references: UNIPROT:Q75760; EMBL:U63632; NID:g1465777; PID:g1465781
;Genetics:
                           Species: human immunodeficiency virus type 1, HIV-1
.Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
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A, Note: sequence extracted from NCBI backbone (NCBIP:117724)
C, Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 176; DB 2;
Pred. No. 1.8e-17;
3; Mismatches 1;
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Pred. No. 2.7e-17;
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                                                                                                          R;Chiodi, F. submitted to the EMBL Data Library, June 1993 A;Reference number: 838800
                                                         Date: 06-Feb-1995 #sequence_revis:
Accession: S35862; S35860; S35863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-110 <MCN>A;Cross-references: UNIPROT: Q9PY06
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Best Local Similarity 88.6%;
Matches 31; Conservative
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A;Accession: T09448
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Best Local Similarity
Matches 31; Conserv
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-77 < CHI>
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A;Molecule type: DNA
A;Residues: 1-77 <CH2>
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A,Cross-references: UNIPROT:Q77541; EMBL:Z21243; NID:g313629; PIDN:CAA80761.1; PID:g31363
C;Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                env protein - human immunodeficiency virus type 1
(Species: human immunodeficiency virus type 1, HIV-1
(C)Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
(C)Accession: S13289
(R)O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
(A) Mature 348, 69-73, 139
(A) A; Title: HIV-1 tropism for monounclear phagocytes can be determined by regions of gpl20 c
A; Reference number: S13288; MUID:91043044; PMID:2172833
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: S35859; S35871
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
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89.7%; Score 175; DB 2; Length 76;
Best Local Similarity 88.6%; Pred. No. 2.5e-17;
Matches 31; Conservative 2; Mismatches 2; Indels
                                                            Indels
                                                                                                                                                           293 CTRPNNNTRKSIHIGPGRAFYTTGEIIGDIRQAHC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 CTRPNNNTRKSIHIGPGRAFYTTGEIIGDIRQAHC 327
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Score 176; DB 2;
Pred. No. 2.2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.3%; Score 176; DB 2;
88.6%; Pred. No. 2.2e-16;
live 3; Mismatches 1
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A;Molecule type: DNA
A;Residues: 1-847 <0BR>
A;Cross-references: UNIPROT:Q75760
C;Superfamily: type E retrovirus env polyprotein
                                                         3; Mismatches
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A;Cross-references: UNIPROT:Q77519; UNIPROT:Q77516; EMBL:Z23216; EMBL:Z23219
C;Superfamily: type E retrovirus env polyprotein
                                                                                                                                    C.Species: human immunodeficiency virus type 1 (fragment)
C.Species: human immunodeficiency virus type 1, HIV-1
C.Species: 0. Feb-1995 #sequence revision 06-Feb-1995 #text_change 09-Jul-2004
C.Accession: S.35834 S.35837
A.Reference number: S.35804
A.Reference number: S.35804
A.Reference number: D.Species: D.Species: D.NA
A.Residues: 1-77 cCHI>
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: S35835
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Pred. No. 4.8e-17;
1; Mismatches 3.
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   43 CIRPNNNTRKSISIGPGRAFYTTGEIIGDIRQAHC 77
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A;Residues: 1-77 -CHI>
A;Cross-references: UNIPROT:Q77517; EMBL:Z23217
C;Superfamily: type E retrovirus env polyprotein
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S35836
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-77 -CHI:
A;Cross-references: UNIPROT:Q77504; UNIPROT:Q77502; EMBL:Z23201; NID:g313548; PIDN:CAA8G
C;Superfamily: type E retrovirus env polyprotein
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A, Molecule type: DNA
A, Residues: 1-443 <BUR>
A, Cross-references: UNIPROT: Q80023, GB:M77230; NID: 9328631; PIDN: AAB03792.1; PID: 9555015
A, Note: this virus was isolated from the mother's sexual partner
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C;Superfamily: type E retrovirus env polyprotein
C;Superfamily: type E retrovirus env polyprotein; glycoprotein; immunodeficiency; polyprote;
C;Reywords: AIDS; capsid protein; cost protein gp120 (fragment) #status predicted <GP1>
F;1252-443/Product: cost protein gp41 (fragment) #status predicted <GP2>
F;252-443/Product: cost protein gp41 (fragment) #status predicted <GP2>
F;424-443/Domain: transmembrane #status predicted <TNN>
F;9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca
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C;Superfamily: type E retrovirus env polyprotein
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Staurger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A;Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A;Reference number: A41621; MUID:92107924; PMID:1763038
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N;Alternate names: coat polyprotein
N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: i1-Feb_1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   envelope protein - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: S35819; S35856
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89.7%; Score 175; DB 2; L
Best Local Similarity 88.6%; Pred. No. 2.5e-17;
Matches 31; Conservative 2; Mismatches 2;
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89.7%; Score 175; DB 2; L
Best Local Similarity 88.6%; Pred. No. 2.5e-17;
Matches 31; Conservative 2; Mismatches 2;
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Best Local Similarity 88.6%; Pred. No. 2.2e-16;
Matches 31; Conservative 2; Mismatches 2;
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submitted to the EMBL Data Library, June 1993
A;Reference number: S35800
A;Accession: S35819
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-77 <CHI>
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Richiodi, F.
submitted to the EMBL Data Library, June 1993
A) Reference number: 835800
A, Accession: 835848
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-77 < CHI>
A, Residues: 1-77 < CHI>
A, Cuss-references: UNIPROT: Q77530; EMBL: Z23232; NID: 9313607; PIDN: CAA80750.1; PID: 93136
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Submitted to the EMBL Data Library, June 1993

Submitted to the EMBL Data Library, June 1993

A.Reference number: 835809

A.Accession: 835849

A.Status: preliminary

A.Status: preliminary

A.Status: preliminary

A.Status: DNA

A.Status: DNA

A.Status: L77 cCHI>

A.Cross-references: UNIPROT:077531; EMBL: 223233; NID:g313609; PIDN:CAA80751.1; PID:g3136

C.Superfamily: type E retrovirus env polyprotein
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 77;
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                        26 CTRPNNNTRKSIHMGPGRAFYATGDIIGDIRQAHC 60
1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC 35
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O78198 PRELIMINARY; PRT; 35 AM.
Q78198;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope protein (Fragment).
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les 35; Conserv
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Copyright (c) 1993 - 2005 Compugen Ltd.
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MEDIJUR=99236722; PubMed=10221533; DOI=10.1089/088922299311088;
Quinnan G.V. Jr., Zhang P.F., Fu D.W., Dong M., Alter H.J.;
Expression and characterization of HIV type 1 envelope protein associated with a broadly reactive neutralizing antibody response.";
AIDS Res. Hum. Retroviruses 15:561-570(1999).
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AF128126; AAD40637.3; -.
HSSP; P04578; 1D1B.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capaid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR000177; GP120.
Pfam; PF00515; GP120.
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                 09dpv9 P
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Envelope protein.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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illarity 100.0%; Pred. No. 4.3e-19;
Conservative 0; Mismatches 0;
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Q9DPW0
Q9DPW1
Q9DPW2
Q9DPW3
Q71020
Q74948
Q40047
Q40047
Q40055
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27 CTRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC 61

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RESULT 4
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GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro: pR000777; GP120.
Pfam; PF00516; GP120; III.
ALDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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MEDIJUE=430197; PubMed=7545939;
Sala M., Zambruno G., Vartanian J., Marconi A., Bertazzoni U.,
Wain-Hobson S.;
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MEDLINE=98242906; PubMed=9583604;
Lukashov V.V., Op de Coul E.L., Coutinho R.A., Goudsmit J.;
"HIV-1 strains specific for Dutch injecting drug users in
heterosexually infected individuals in The Netherlands.";
AIDS 12:635-641(1998).
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Best Local Similarity 97.1%; Pred. No. 9.9e-20;
Matches 34; Conservative 1; Mismatches 0; Indels
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91 AA; 10363 MW; 0D9690FAZ767592E CRC64;
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GO; GO:0019028; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000777; GP120.
InterPro; IPR011056; Pept_S24_S26_C.
Pfam; PF00516; GP120; 1.
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                                luman immunodeficiency virus 1.
//ruses; Retroid viruses; Retroviridae; Lentivirus.
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les 34; Conservative
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EMBL; Z34376; CAA84146.1;
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                                                                                             NCBI_TaxID=11676;
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"HIV type 1 subtypes in The Netherlands circulating among women originating from AIDS-endemic regions.";

AIDS Res. Hum. Retroviruses 12:951-953(1996).

EMBL, L76886; AAC37946.1; -..

EMBL, L76886; AAC37946.1; -..

GO, GO:0019028; C:integral to membrane; IEA.

GO, GO:0019028; C:viral capsid; IEA.

GO, GO:0019028; F:structural molecule activity; IEA.

InterPro; IPR000777; GP120.

Pfam; PR00516; GP120;

Pfam; PR00516; GP120;

Pfam; PR00516; GP120;

ADDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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EMBL, AJ228189; CAA12819.1; --
GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0019028; C:viral capsid; IEA.

GO, GO:0019031; C:viral envelope; IEA.

GO, GO:0019031; C:viral mivelope; IEA.

InterPro; IPR000777; GP120.
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                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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AIDS; Coat protein; Glycoprotein; Transmembrane.
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MEDLINE=96392168; PubMed=8798980;
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Wang X.-P., Kahn P.D., Cunha C.B., Dosik D.A., Gawel C., Kaplan M.H.;

Wang X.-P., Kahn P.D., Cunha C.B., Dosik D.A., Gawel C., Kaplan M.H.;

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AX375253; AAG83712.1; -.

GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0019031; C:viral envelope; IEA.

GO, GO:0015081; E:structural molecule activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buropean injecting drug users seroconverting from 1984 to 1997."; AIDS 15:257-266(2001).
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:001908; F:structural molecule activity; IEA.
InterPro; IPR000777; GP120.
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
Query Match 96.9%; Score 189; DB 2; I
Best Local Similarity 94.3%; Pred. No. 2.5e-19;
Matches 33; Conservative 2; Mismatches 0;
                                                                                         1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC 35
                                                                                                                    96.9%; Score 189; DB 2;
94.3%; Pred. No. 2.6e-19;
iive 2; Mismatches 0
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MEDLINE=21084776; Pubmed=11216936;
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es 33; Conservative
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"HIV type 1 V3 variation dynamics in vivo:long-term persistence of non-syncytium-inducing genotypes and translent presence of cyncytium-inducing genotypes and translent presence of cyncytium-inducing genotypes and translent presence of cyncytium-inducing genotypes during the course of progressive AIDS.";
AIDS Res. Hum. Retroviruses 13:1597-1609(1997).
EMBL; AB005412; BAA3329.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid, IEA.
GO; GO:0019031; C:viral molecule activity; IEA.
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InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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InterPro; IPR011056; Pept_S24_S26_C.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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171 AA; 18865 MW; 46C82EDEFBADEBOB CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                    85 CSRPNNNTRKSIPMGPGKAFYTTGEIIGDIRQAHC 119
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                                                                                                                                                                                                    Ouery Match 96.9%; Score 189; DB 2; Best Local Similarity 94.3%; Pred. No. 5.3e-19; Matches 33; Conservative 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                         1 CSRPNNNTRKSIPMGPGRAFYTTGQIIGDIRQAHC 35
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Pred. No. 1.3e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        091430 PRELIMINARY; PRT; 091430; 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last seq
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MEDLINE=98090117; Pubmed=9430252;
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"Spatial discontinuities in human immunodeficiency virus type 1 quasispecies derived from epidermal Langerhans cells of a patient with AIDS and evidence for double infection.";
J. Virol. 68:5280-5283 (1994).

EMBL; Z34437; CAA84207.1; CAA84207.1;
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000777; GD120.
InterPro; IPR011056; Pept_S24_S26_C.
Pfam; PF00516; GP120; 1.
PAIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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"Spatial discontinuities in human immunodeficiency virus type 1
"Spatial discontinuities in human immunodeficiency virus type 1
quasispecies derived from epidermal Langerhans cells of a patient with
AIDS and evidence for double infection.";
J. Virol. 68:5280-5283 (1994).

EMBL; Z34435; CAA84205.1; -.
EMBL; Z34435; CAA84205.1; -.
EMBC; Z34435; CAA84205.1; -.
EMBL; Z34435; CAB84205.1; -.
InterPro; IPR010105; Pept S24_S26_C.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                       TISSUE-Epidermis;
MEDLINE-94309197; PubMed=7545939;
Sala M., Zambruno G., Vartanian J., Marconi A., Bertazzoni U.,
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MEDLINE=94309197; PubMed=7545939;
Sala M., Zambruno G., Vartanian J., Marconi A., Bertazzoni U.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 35 AA; 3857 MW; 9F5A5B2A698BF77E CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Envelope protein (Fragment).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                            Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
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Best Local Similarity 94.5.,
Conservative
Conservative
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Matches 33; Conservative
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                               NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Wain-Hobson S.;
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05-JUL-2004
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                                                                                                                                         "Spatial discontinuities in human immunodeficiency virus type 1
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                  MEDLINE-94309197; PubMed-7545939;
Sala M., Zambruno G., Vartanian J., Marconi A., Bertazzoni U.,
Wain-Hobson S.;
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MEDLINE=94309197; PubMed=7545939;
Sala M., Zambruno G., Vartanian J., Marconi A., Bertazzoni U.,
Wain-Hobson S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.4%; Score 188; DB 2; Length 35; 94.3%; Pred. No. 1.3e-19; tive 2; Mismatches 0; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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NCBI_TaxID=11676;
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GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000777; GP120.
InterPro; IPR011056; Pept S24_S26_C.
Pfam; PF00516; GP120.
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Matches 33; Conservative
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TISSUE~Epidermis;
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Q76PM1
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Q76PM1; 05-JUL-2004 (TrEMBLrel. 27, Created)

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33; Conservative
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SEQUENCE
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Q76PM5
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"Spatial discontinuities in human immunodeficiency virus type 1
"Spatial discontinuities in human immunodeficiency virus type 1
quasispecies derived from epidermal Langerhans cells of a patient with
AIDS and evidence for double infection.";
J. Virol. 68:5280-5283(1994).
EMBL; 234437; CAA94202.1; -
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR01075; GPL20.
InterPro; IPR011056; Pept_S24_S26_C.
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EMBL; Z3443; CAA84203.1; -.

CO, GO:0019031; C:viral envelope; IEA.

InterPro; IPR011056; Pept_S24_S26_C.

Pfam; PF00516; GP120; 1.

Pfam; PF00516; GP120; 1.

AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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MEDLINE=94309197; PubMed=7545939;
Sala M., Zambruno G., Vartanian J., Marconi A., Bertazzoni U.,
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Envelope protein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Pred. No. 1.3e-19;
2; Mismatches 0;
1 CTRPNNNTRKSIPIGPGRAFYTTGQIIGDIRQAHC 35
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MEDLINE=94309197; PubMed=7545939;
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Local Similarity 94.3%;
les 33; Conservative
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AIDS and evidence for double infection.";
EMBL: 234430; CAA84200.1;
EMBL: 234430; CAA84200.1;
InterPro; IPRO00777; GP120.
InterPro; IPRO1056; Pept_S24_S26_C.
Pfam; PF00516; GP120; 1.
PAIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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MEDLINE=9430917; PubMed=7545939;
Sala M., Zambruno G., Vartanian J., Marconi A., Bertazzoni U.,
Wain-Hobson S.;
                                                                                           Score 188; DB 2; Length 35;
Pred. No. 1.3e-19;
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35 AA; 3857 MW; 9F5A5B2A69BBF77E CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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                                                                    Query Match
Best Local Similarity 94.3%,
Best Local 33; Conservative
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